

GenCore version 5.1.7  
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## OM protein - protein search, using sw model

Run on: March 2, 2006, 03:53:56 ; Search time 48 Seconds  
(without alignments)  
1216.021 Million cell updates/sec

Title: US-10-755-889-18

Perfect score: 3793 1 MASPADSCIOFTRHSDVLI.....TKVQYVSATDLPPELPKAC 706

Sequence: 1 MASPADSCIOFTRHSDVLI.....TKVQYVSATDLPPELPKAC 706

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database:

Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/6.COMB.pep.\*  
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4: /cgn2\_6/ptodata/1/1aa/PTCUS.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/RE.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiletest.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	3777	99.6	706 2 US-09-538-092-1104	Sequence 1104, Ap
2	3763	99.2	706 1 US-08-074-967-2	Sequence 2, Appli
3	3763	99.2	706 1 US-08-553-541B-2	Sequence 2, Appli
4	3763	99.2	706 2 US-09-268-202-2	Sequence 2, Appli
5	3763	99.2	706 2 US-09-761-117-2	Sequence 2, Appli
6	3763	99.2	706 4 PCT-US94-06669-2	Sequence 2, Appli
7	602	15.9	803 2 US-09-063-035-2	Sequence 2, Appli
8	560	14.8	110 1 US-08-553-541B-9	Sequence 9, Appli
9	560	14.8	110 1 US-09-268-202-9	Sequence 9, Appli
10	540	14.2	733 2 US-09-761-117-9	Sequence 7651, Ap
11	540	14.2	733 2 US-09-949-016-7651	Sequence 10, Appli
12	538	14.2	106 1 US-08-340-203A-10	Sequence 10, Appli
13	538	14.2	106 1 US-08-452-427-10	Sequence 10, Appli
14	538	14.2	106 1 US-08-085-407-10	Sequence 10, Appli
15	508	13.4	678 2 US-09-949-016-10273	Sequence 10273, A
16	503	13.3	799 2 US-10-104-047-2929	Sequence 2929, Ap
17	501	13.2	673 2 US-09-538-092-1270	Sequence 1270, Ap
18	483	12.7	488 1 US-08-933-750C-17	Sequence 17, Appli
19	483	12.7	488 2 US-09-234-613-17	Sequence 17, Appli
20	481	12.7	685 2 US-09-949-016-8627	Sequence 8627, Ap
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24	476	12.5	458 2 US-09-538-092-1356	Sequence 1356, Ap
25	469	12.4	541 2 US-10-104-047-2161	Sequence 2161, Ap
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45	442	11.7	292 2 US-09-538-092-1334	Sequence 1334, Ap

## ALIGNMENTS

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RESULT 1
US-09-538-092-1104
Sequence 1104, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glot, Loic
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: Curabatsqformat Version 0.9
SEQ ID NO 1104
LENGTH: 706
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc:feature
LOCATION: (0)..(0)
OTHER INFORMATION: Polypeptide Accession Number P41182
US-09-538-092-1104
Query Match 99.6%; Score 3777; DB 2; Length 706;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 703; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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DB 361 SPKAPSPDPKACNMKKYKFIVLNSLNONAKPGPBOAELGRLSPRAYTAPACOPMPER 420
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DB 421 ENIDLOSPTKLASGSDSTIPQASRLNNIVNRSMTGSPSSSSSHPLVMPKCTSCS 480
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DB 661 EKCNLHFRHKSQRLRLRQKGAIITWTKQYRVSATDLPPELPKAC 706

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## RESULT 2

US-08-074-967-2

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; Sequence 2, Application US/08074967
; Patent No. 5641672

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## GENERAL INFORMATION:

APPLICANT: Dalia-Favera, Riccardo

APPLICANT: Chaganti, R.S.K.

TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS

TITLE OF INVENTION: bcl-6

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSER: Cooper &amp; Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/074,967

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/43771

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 706 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-074-967-2

Query Match 99.2%; Score 3763; DB 1; Length 706;

Best Local Similarity 99.3%; Pred. No. 0;  
Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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DB 121 CKKFKASAEAVSAIKPREFFLNSRMLMPDIDIAVYGRVENVNLPKRSAPGESAF 180
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## RESULT 3

US-08-553-541B-2

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; Sequence 2, Application US/08553541B
; Patent No. 5882858

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## GENERAL INFORMATION:

APPLICANT: Dalia-Favera, Riccardo

APPLICANT: Chaganti, Raju S.K.

TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS

TITLE OF INVENTION: bcl-6

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSER: Cooper &amp; Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

US-08-553-541B-2

SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/553,541B  
 FILING DATE: May 28, 1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 391-0525  
 TELEFAX: (212) 391-0525  
 TELETYPE: 422523 COOP UI  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 706 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-553-541B-2

Query Match 99.3%; Score 3763; DB 1; Length 706;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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## RESULT 4

US-09-268-202-2

Sequence 2, Application US/09268202

Patent No. 6174997

GENERAL INFORMATION:

APPLICANT: Dalia-Favera, Riccardo

TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS

TITLE OF INVENTION: bcl-6

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSER: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

Application Number: US/09/268,202

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 391-0525

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 706 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-268-202-2

Query Match 99.2%; Score 3763; DB 2; Length 706;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 MASPADSCIOFTRHARVDLNLNLRSDILTDVVIIVSREOFRAHKTIVMACSGLFYSI 60  
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Db 361 SPPAKSPDTPKACSMKKYKFIVLNSLNQNAKPGGPEQAEGLSPRAYTAPACQPMMP 420
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Db 421 ENLDLQSPTKLASGSDSTTPQASRLNNIYNRSMTGSPRSSSESHSPLYMHPKCTSCGS 480
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Db 481 OSPOHAEMLHTAGTFAEMGETOSEYSDSCENGAFPCNECDGCFSEBASLKHHTLTOT 540
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Db 661 EKCNLFHRKSQLRLHROKGAITNTKVQYVSATDLPPELPKAC 706

RESULT 5
US-09-761-117-2
; Sequence 2, Application US/09761117
; Patent No. 6783945
; GENERAL INFORMATION:
; APPLICANT: Dalia-Favera, Riccardo
; TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/761,117
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX: 422523 COOP UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 706 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-761-117-2

Query Match 99.2%; Score 3763; DB 2; Length 706;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MASPADSCIOFTIRASDVLTNLNRLRSRDILTVDVIVVSHQOPRAKTVLMACSGLYFSI 60
Db 1 MASPADSCIOFTIRASDVLTNLNRLRSRDILTVDVIVVSHQOPRAKTVLMACSGLYFSI 60

```

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Qy 61 FTDLKCNLSVTNLDPEINPBGFCILDFMTYSRLNLRBNIMAYMATAMYLQMEHVDT 120
Db 61 FTDLKCNLSVTNLDPEINPBGFCILDFMTYSRLNLRBNIMAYMATAMYLQMEHVDT 120
Qy 121 CRKFIKASAEWVSAIKPREEFLNLRMLPQDIMAAYGREVENNLPJRSAPGCEBAF 180
Db 121 CRKFIKASAEWVSAIKPREEFLNLRMLPQDIMAAYGREVENNLPJRSAPGCEBAF 180
Qy 181 APSLYGSLSTPPASYSMTSHLPVSSLFSDDEFRRVMPVNPFPKRALPCDSARPVPG 240
Db 181 APSLYGSLSTPPASYSMTSHLPVSSLFSDDEFRRVMPVNPFPKRALPCDSARPVPG 240
Qy 241 EYSRPTLWSPVNCNSIYSPKETIPEARSQPMHVSVAEGLKPAAPSAANAPFCPCDAS 300
Db 241 EYSRPTLWSPVNCNSIYSPKETIPEARSQPMHVSVAEGLKPAAPSAANAPFCPCDAS 300
Qy 301 KEERPPSSEDEIALHFEPPNAPLNKGLVSPQSPKSDCQNSPTBACSSKNACILQASG 360
Db 301 KEERPPSSEDEIALHFEPPNAPLNKGLVSPQSPKSDCQNSPTBACSSKNACILQASG 360
Qy 361 SPPAKSPDTPKACSMKKYKFIVLNSLNQNAKPGGPEQAEGLSPRAYTAPACQPMMP 420
Db 361 SPPAKSPDTPKACSMKKYKFIVLNSLNQNAKPGGPEQAEGLSPRAYTAPACQPMMP 420
Qy 421 ENLDLQSPTKLASGSDSTTPQASRLNNIYNRSMTGSPRSSSESHSPLYMHPKCTSCGS 480
Db 421 ENLDLQSPTKLASGSDSTTPQASRLNNIYNRSMTGSPRSSSESHSPLYMHPKCTSCGS 480
Qy 481 OSPOHAEMLHTAGTFAEMGETOSEYSDSCENGAFPCNECDGCFSEBASLKHHTLTOT 540
Db 481 OSPOHAEMLHTAGTFAEMGETOSEYSDSCENGAFPCNECDGCFSEBASLKHHTLTOT 540
Qy 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTEKPEYRCNICGAOPNRPANLKTTHRIHSGEK 600
Db 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTEKPEYRCNICGAOPNRPANLKTTHRIHSGEK 600
Qy 601 PYCETCGARFQVAVHLRAHVLHTGEKPYPCICGTRPRHLQTLKSHLRHTGKPYHC 660
Db 601 PYCETCGARFQVAVHLRAHVLHTGEKPYPCICGTRPRHLQTLKSHLRHTGKPYHC 660
Qy 661 EKCNLFHRKSQLRLHROKGAITNTKVQYVSATDLPPELPKAC 706
Db 661 EKCNLFHRKSQLRLHROKGAITNTKVQYVSATDLPPELPKAC 706

RESULT 6
PCT-US94-06669-2
; Sequence 2, Application PC/TUS9406669
; GENERAL INFORMATION:
; APPLICANT: Dalia-Favera, Riccardo
; APPLICANT: Chaganti, R.S.K.
; TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06669
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/074,967

```



FILING DATE: 09-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 43771-A-PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 977-9550  
 TELEFAX: (212) 664-0525  
 TELE: 422523 COOP UI  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 706 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US94-06669-2

Query Match 99.2%; Score 3763; DB 4; Length 706;  
 Best Local Similarity 99.3%; Pred. No. 0;  
 Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASPDSCIOFTRHSDVNLNLRSGDILTDVIVVSREOPRAHKTVMACSGLFYSI 60  
 DB 1 MASPDSCIOFTRHSDVNLNLRSGDILTDVIVVSREOPRAHKTVMACSGLFYSI 60  
 QY 61 FTDQKCNLSVINLDPINPEGFCILLDMYTSRLNREGNIMAVMATYLOMEHVDI 120  
 DB 61 FTDQKCNLSVINLDPINPEGFCILLDMYTSRLNREGNIMAVMATYLOMEHVDI 120  
 QY 121 CRKFKASAEAMWSAIPREBEFLNSRLMPODIMAYRGREVENNIPLSAPGCEERAF 180  
 DB 121 CRKFKASAEAMWSAIPREBEFLNSRLMPODIMAYRGREVENNIPLSAPGCEERAF 180  
 QY 121 CRKFKASAEAMWSAIPREBEFLNSRLMPODIMAYRGREVENNIPLSAPGCEERAF 180  
 DB 121 CRKFKASAEAMWSAIPREBEFLNSRLMPODIMAYRGREVENNIPLSAPGCEERAF 180  
 QY 181 APSLYSGISTPPASVYSHLPVSSLFSDSEFRDVMVPANPPKERRALPCDSARVPVG 240  
 DB 181 APSLYSGISTPPASVYSHLPVSSLFSDSEFRDVMVPANPPKERRALPCDSARVPVG 240  
 QY 241 EYSRPTLEVPNVCHSNISPKETIPREASDMHYSAEGLKPAAPARNAVPFPCDKAS 300  
 DB 241 EYSRPTLEVPNVCHSNISPKETIPREASDMHYSAEGLKPAAPARNAVPFPCDKAS 300  
 QY 301 KEERPSSEDEIALHFEPPNAPLNKGLVSPQSKDCOPNSTEACSSKNAICILQASG 360  
 DB 301 KEERPSSEDEIALHFEPPNAPLNKGLVSPQSKDCOPNSTEACSSKNAICILQASG 360  
 QY 361 SPPAKSPDPPKACMKKKYKFTVNSLNQNAKPGPEQAEIGRLSPRAYTAPACOPMPER 420  
 DB 361 SPPAKSPDPPKACMKKKYKFTVNSLNQNAKPGPEQAEIGRLSPRAYTAPACOPMPER 420  
 QY 421 ENLLOSPTRLKASGEBSTIPQASRLNNIVNRSMTGSPRSSSESHSPLYMHPPKCTSGS 480  
 DB 421 ENLLOSPTRLKASGEBSTIPQASRLNNIVNRSMTGSPRSSSESHSPLYMHPPKCTSGS 480  
 QY 481 QSPHAEMCLHTAGPTFAEMWGETQSEYSDSSCENGAFFCNECDRCRSEASLKRHTLOT 540  
 DB 481 QSPHAEMCLHTAGPTFAEMWGETQSEYSDSSCENGAFFCNECDRCRSEASLKRHTLOT 540  
 QY 541 HSDPYKCDRCOASFRYKGNLASHKTVTGKPRCNICGAOFNRPALKTHTTHISEK 600  
 DB 541 HSDPYKCDRCOASFRYKGNLASHKTVTGKPRCNICGAOFNRPALKTHTTHISEK 600  
 QY 601 PYKETCGARFVQVAHJLAHVLHTGKPYCEICGTRFRHLQTLKSLRHTGKPYHC 660  
 DB 601 PYKETCGARFVQVAHJLAHVLHTGKPYCEICGTRFRHLQTLKSLRHTGKPYHC 660  
 QY 661 EKNLHFRHKSQRLHLRQKGAITNTVQYRVASATDLPPLPKAC 706  
 DB 661 EKNLHFRHKSQRLHLRQKGAITNTVQYRVASATDLPPLPKAC 706

RESULT 7  
 US-09-063-035-2  
 Sequence 2, Application US/09063035

Patent No. 616091  
 GENERAL INFORMATION:  
 APPLICANT: PECKERT, Karen; HAENEL, Frank; and EILERS,  
 APPLICANT: Martin  
 TITLE OF INVENTION: Myc-binding zinc finger proteins,  
 TITLE OF INVENTION: their preparation and their use  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Keil & Weinlauf  
 STREET: 1101 Connecticut Avenue  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.2 Mb storage  
 COMPUTER: IBM AT-compatible, 80486 processor  
 OPERATING SYSTEM: MS-DOS version 6.1  
 SOFTWARE: Wordperfect version 8.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/063,035  
 FILING DATE: 21-Apr-1998  
 CLASSIFICATION: 514  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 803 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-09-063-035-2

Query Match 15.9%; Score 602; DB 2; Length 803;  
 Best Local Similarity 26.2%; Pred. No. 2.2e-45; Indels 156; Gaps 23;  
 Matches 196; Conservative 100; Mismatches 297;

QY 9 IOFTRHSDVNLNLRSGDILTDVIVVSREOPRAHKTVMACSGLFYSITDQKCN 68  
 DB 1 MDPPQSHVLEBINOQROGLDCTFVVDGVHFAHKAVALAACSEYFGMLFVDQ 56  
 QY 69 LSVINLDPINPEGFCILLDMYTSRLNREGNIMAVMATYLOMEHVDTCRKFKAS 128  
 DB 57 KDVVHLDIS-NAAGLQMLEFMTAKLSLSPENVVDVLAVALTLOMODITACHALKSLA 115  
 QY 129 EAMWSAIPREBEFLNSRLMPODIMAYRGREVENNIPLSAPGCEERAF 184  
 DB 116 E-PATSP-----GNAEALATBEGGDKKAKBEKVATST 146  
 QY 185 YS-----GLSTP--PASVYSHLPVSSLFSDSEFRDVMVPANPPKERRALPCDSARP 237  
 DB 147 LSRLEQAGNSTPIGPS-----RDLK-----ERCGQAQSAAS 178  
 QY 238 VPGEYSRPTLEVPNVCHSNISPKETIPREASDMHYSAEGLKPAAPARNAVPFPCD 297  
 DB 179 GAGOTERAD-----APREPPVELKPDPTSGMAAABAEALSSSQEWEVE 225  
 QY 298 KASKEERPSSEDEIALHFEPPNAPLNKGLVSPQSKDCOPNSTEACSSKNAICILQASG 355  
 DB 226 PARKGEERKEOEQEEBAGAP-AEVKESQOLENGEABENEBEAGAGDSQGLGS-- 282  
 QY 356 LQASG--SPPAKSPDPPKACMKKKYKFTVNSLNQNAKPGPEQAEIGRLSPRAYTAPACOPMPER 406  
 DB 283 -EARGLSRGYGDRTESKAAGSVYHKCEDGKEFTHTGNKRHRIRITGKPEPCRCCKSK 341  
 QY 407 AYTAAPACOPMPERENLQSPTRLKASGEBSTIPQASRLNNIVNRSMTGSPRSSSESHS 466  
 DB 342 AFSDPAKAC-----AHEKTHSLPKPYGCECGKSYRLISLNLHKKHSGEABARYRCDCG 396  
 QY 467 PLY-----MH-----PPKCTSGSGSPQHAEMCLHTAGPTFAEMWGETQSEYSDS 511  
 DB 397 KLFTTSGNLKRHOVLHSGEKPYQCDYCGRFSPTSGRHL-----ETHDIDKEXKCP 449  
 QY 512 SCE-----NGAFCNECDRCRSEASLKRHTLOTSH-DKPYKCDRCQ 552  
 DB 450 HCDKKFQVGNLKAHLKIHLADGFLKCRBEGKQPTTSGNLKRO-LRHSGEKPYVCIHQ 508

Oy	553	ASFRYKGNLASHHTVITGEKPYRCN CGAQFNRPA LTRHINSGEKPYCEICGARFV	61.2
Db	509	RQFDPCALORRHRIHTGEPCCVCWAGAF OASSL AHARQHTEKPYCEICGARFV	56.8
Oy	613	QVAHLRAHVLIHTGEKPYCEICGRFRIQT KSHRLIHTGEKPYCEHCENL FRRKSQ	67.2
Db	569	QSGLANHIHHNNIRPHKCVCSKA FVVGNLS HIIITHTEKPYLDCKGGRGFNRVDN	62.8
Oy	673	LRLTRKHGAITNTKVQYRVSATDLPPE	70.1
Db	629	LRSIVKTVMQGAKIGIKI-----LEPE	64.9

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US-08-553-541B-9
US-08-553-541B-9
; Sequence 9, Application US/08553541B
; Patent No. 5882858
; GENERAL INFORMATION:
; APPLICANT: Dalla-Favera, Riccardo
; APPLICANT: Chaganti, Raju S.K.
; TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
; TITLE OF INVENTION: bcl-6
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,541B
; FILING DATE: May 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-553-541B-9

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Query Match 14.8%; Score 560; DB 1; Length 110;
Best Local Similarity .99.1%; Pred. No. 6,3e-43;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

QY      8 CIOFRRHSDVLTNLTNRLRSRDILTDDVTVVRSBQFRAKTVLMCSGLFYSPTDOLKC 67
       1 CIOFRRHSDVLTNLTNRLRSRDILTDDVTVVRSBQFRAKTVLMCSGLFYSPTDOLKC 60

QY      68 NLSVTNLPDPEINPEGFCILADEMYTSRLTLRGKINMAVMAATAMYLOMEHV 117
       61 NLSVTNLPDPEINPEGFCILADEMYTSRLTLRGKINMAVMAATAMYLOMEHV 110

Db

RESULT 9
US-09-268-202-9
; Sequence 9, Application US/09268202

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Patent No. 6174997  
GENERAL INFORMATION:  
APPLICANT: Dalla-Favera, Riccardo  
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS  
TITLE OF INVENTION: bcl-6  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/268,202  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-268-202-9

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Query Match          14.8%; Score 560; DB 2; Length 110;
Best Local Similarity 99.1%; Pred. No. 6,3e-43;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy      8 CIGTTRASDVLTNLNLRISRDIITDVIVVSREQFAHKVTLMACSGLFYSITDOLKC 67
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1 CIGTTRASDVLTNLNLRISRDIITDVIVVSROFPAHKVTLMACSGLFYISITDOLKC 60
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

        68 NLASYINIDPEINPEGFCILDFMTYSTRNLREGIMAVMATMYLQMEHV 117
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
        61 NLSVINIDPEINPEGFCILDFMTTSRLNLRGINMAVMATMYLQMEHV 110
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 10
US-09-761-117-9
Sequence 9, Application US/09761117
Patent No. 6783945

GENERAL INFORMATION:
APPLICANT: Dalia-Favera, Riccardo
Chaganti, Raju S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
                bcl-6
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/761,117  
FILING DATE: 16-Jan-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 110 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-761-117-9

Query Match 14.8%; Score 560; DB 2; Length 110;  
Best Local Similarity 99.1%; Pred. No. 6.3e-43;  
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 8 CIOFTRASDVLTNLRSLDITDVIVVSRQFRAHKTVMACGLFYISITDOLK 67  
1 CIOFTRASDVLTNLRSLDITDVIVVSRQFRAHKTVMACGLFYISITDOLK 60

Qy 68 NLAVINDPEINPEGFCILDFMTSLRLREGNIMAVMATYLMQEHV 117  
61 NLAVINDPEINPEGFCILDFMTSLRLREGNIMAVMATYLMQEHV 110

Db 61 NLAVINDPEINPEGFCILDFMTSLRLREGNIMAVMATYLMQEHV 110

RESULT 11  
US-09-949-016-7651  
Sequence 7651, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7651  
LENGTH: 733  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-7651

Query Match 14.2%; Score 540; DB 2; Length 733;  
Best Local Similarity 25.0%; Pred. No. 8e-40;  
Matches 190; Conservative 103; Mismatches 270; Indels 196; Gaps 29;

Qy 11 FTRNASDVLTNLRSLDITDVIVVSRQFRAHKTVMACGLFYISITDOLK 70  
50 FTRNASDVLTNLRSLDITDVIVVSRQFRAHKTVMACGLFYISITDOLK 108  
71 VINDPRIINPEGFCILDFMTSLRLREGNIMAVMATYLMQEHV 126  
109 VINDPRIINPEGFCILDFMTSLRLREGNIMAVMATYLMQEHV 159

127 ASBAENVSAIKPREEFLNSRMLPQDIMAYRGREVENNLPLRSAPGESRAFAPIYS 186  
160 -----KP-----KTSVGOAAGQ-----S 173  
187 GLSTPASYSMYSHLPSVSLFSDBEFVDVMEVNPFPKRALPCDSARPVGEYSRPT 246  
174 GLG-PPASQVNSHVKEPAGLEBEVSRTGL-----VPDQE-PRGSHSP-----ORPQ 221  
247 LEVSPVNCNSNIYSPKETTPEEKASDMYHVAEGLKPA-----APBARNAFPPOCKASK 301  
222 L-----HSPAQOS-----EGPSSICGLKQALPCPLEDKKPPBDCKVPPPLEEGA 267  
302 EEEPPSSEDEIALHFE-----PPNAPLNKGLVPSQSPKSCQOPSPTACSSKN 352  
268 QLOGGSNEVEVVQVEDDGDGYMSPEAVLTR-----KSNVIRKPCAAB 314  
353 ACILQASGSPPAKS-----PTDPKACNMK-----KYRETVLNSINQAKPGAPQABIGRL 403  
315 ALSAGSLAEPAPENRKGTAVPVBCPTCHKKFLSKYLLKVNRRKHTEKEP----- 363  
404 SPRAYTAPPAQOPMEPENIDLOSPTKLSASGEDSTTPQASRLNIVNRS-----MTGSP-- 458  
364 -----FECPKCKCYFRKENTL-----LEHEAR--NCMNRESEOVFTCSVCQ 401  
459 -----RSSSESHSPLYM-----PPKCTSCGSGSPQHAEMCLHT-----AGPTFAE-E 500  
402 ETRRRRMELRVHNVSHTEGMEPYRSCSQOPWCKKQDQSMITLHGAPKPAHACTCAKCF 461  
501 MGETOSEYSDSCENG--AFPCNECDRPFSEASLKRHTLOT-SDPYKCDRCQASFRY 557  
462 LSRTEQLHAFKRGKEKLFVCECGHRASRNGLOMHTAKRNRBPHCECSNAFTQ 521  
558 KGNLASHKTVHTEKEPYRCNICGAOFNRPANLKTHTRIHSGEYKCEYTCGAPFVQYAH 617  
522 KANLNHMLRHTGEKEPQCHLCKTFRQASLDKRNRTHTGERPFSCPEORFTEKGPL 581  
618 RAHVLI-HTGEKYPCEICGTRPRHLOTLKSHLRHTGEKYPHCEKCNLHFRKSOURLH 676  
582 LRHVASHROGRPHFCOICGTEKFAVQLEHVRRHGVKFECTECGYKFRQAHLRH 641  
677 LRQKGAITNTKYQYR-----VSATDLPPEL 702  
642 M-ETHREVENYNPQRKLRNLIIEDKAMVVVALQPPAEL 679

Db 677 LRQKGAITNTKYQYR-----VSATDLPPEL 702  
642 M-ETHREVENYNPQRKLRNLIIEDKAMVVVALQPPAEL 679

Qy 677 LRQKGAITNTKYQYR-----VSATDLPPEL 702  
642 M-ETHREVENYNPQRKLRNLIIEDKAMVVVALQPPAEL 679

RESULT 12  
US-08-340-203A-10  
Sequence 10, Application US/08340203A  
Patent No. 5756668  
GENERAL INFORMATION:  
APPLICANT: Baylin, Stephen B.  
APPLICANT: Wales, Michele M.  
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, HIC-1  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: California  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/340,203A  
FILING DATE: 15-NOV-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Ph.D., Lisa A.

REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: 07265/039001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-340-203A-10

Query Match 14.2%; Score 538; DB 1; Length 106;  
Best Local Similarity 100.0%; Pred. No. 5.9e-41;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TRHSDVLTNLRSLRSDILTDVIVVSRQFRAKTVLMACSGLFYSIFTDQKCNLSV 71  
DB 1 TRHSDVLTNLRSLRSDILTDVIVVSRQFRAKTVLMACSGLFYSIFTDQKCNLSV 60  
QY 72 INLDPEINPEGFCILLDFMTSRLNLRGNIMAVMATMYLQMEHV 117  
DB 61 INLDPEINPEGFCILLDFMTSRLNLRGNIMAVMATMYLQMEHV 106

RESULT 13  
US-08-452-427-10  
Sequence 10, Application US/08452427  
Patent No. 5922590  
GENERAL INFORMATION:  
APPLICANT: Baylin, Stephen B.  
APPLICANT: Wales, Michele M.  
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, HIC-1  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: California  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,427  
FILING DATE: 26-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/340,203  
FILING DATE: 15-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Halie, Ph.D., Lisa A.  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: 07265/039001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-452-427-10

Query Match 14.2%; Score 538; DB 1; Length 106;  
Best Local Similarity 100.0%; Pred. No. 5.9e-41;

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 12 TRHSDVLTNLRSLRSDILTDVIVVSRQFRAKTVLMACSGLFYSIFTDQKCNLSV 71  
DB 1 TRHSDVLTNLRSLRSDILTDVIVVSRQFRAKTVLMACSGLFYSIFTDQKCNLSV 60  
QY 72 INLDPEINPEGFCILLDFMTSRLNLRGNIMAVMATMYLQMEHV 117  
DB 61 INLDPEINPEGFCILLDFMTSRLNLRGNIMAVMATMYLQMEHV 106

RESULT 14  
US-09-085-407-10  
Sequence 10, Application US/09085407  
Patent No. 6103877  
GENERAL INFORMATION:  
APPLICANT: Baylin, Stephen B.  
APPLICANT: Wales, Michele M.  
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, HIC-1  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: California  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/085,407  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/340,203  
FILING DATE: 15-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Halie, Ph.D., Lisa A.  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: 07265/039001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: No. 6103877 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-085-407-10

Query Match 14.2%; Score 538; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 5.9e-41;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TRHSDVLTNLRSLRSDILTDVIVVSRQFRAKTVLMACSGLFYSIFTDQKCNLSV 71  
DB 1 TRHSDVLTNLRSLRSDILTDVIVVSRQFRAKTVLMACSGLFYSIFTDQKCNLSV 60  
QY 72 INLDPEINPEGFCILLDFMTSRLNLRGNIMAVMATMYLQMEHV 117  
DB 61 INLDPEINPEGFCILLDFMTSRLNLRGNIMAVMATMYLQMEHV 106

RESULT 15  
US-09-949-016-10273  
Sequence 10273, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:



**This Page Blank (uspto)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2006, 04:07:37 ; Search time 21 Seconds  
(without alignments)  
672.386 Million cell updates/sec

Title: US-10-755-889-18

Perfect score: 3793  
Sequence: 1 MSPADSCIOFTTHASDVLL.....TKVQYRVASATDLPPELPKAC 706

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 135339 seqs, 20000136 residues

Total number of hits satisfying chosen parameters: 135339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

Published Applications AA-New:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/PC1\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep:\*  
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7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	503	13.3	799	US-11-072-512-2929	Sequence 2929, Ap
2	469	12.4	541	US-11-072-512-2161	Sequence 2161, Ap
3	468.5	12.4	540	US-11-072-512-3748	Sequence 3748, Ap
4	465.5	12.3	781	US-11-072-512-2937	Sequence 2937, Ap
5	465	12.3	586	US-11-072-512-2592	Sequence 2592, Ap
6	463	12.2	556	US-11-072-512-3914	Sequence 3914, Ap
7	458.5	12.1	530	US-11-072-512-2805	Sequence 2805, Ap
8	458	12.1	530	US-11-072-512-3434	Sequence 3434, Ap
9	457	12.0	409	US-11-072-512-2663	Sequence 2663, Ap
10	457	12.0	475	US-11-072-512-3470	Sequence 3470, Ap
11	455	12.0	429	US-11-072-512-2786	Sequence 2786, Ap
12	454.5	12.0	504	US-11-072-512-2053	Sequence 2053, Ap
13	454	12.0	636	US-11-072-512-2449	Sequence 2449, Ap
14	452	11.9	500	US-10-517-151-4	Sequence 4, Appl1
15	445	11.7	643	US-11-072-512-2241	Sequence 2241, Ap
16	442.5	11.7	592	US-11-072-512-3366	Sequence 3366, Ap
17	442	11.7	543	US-11-072-512-3461	Sequence 3461, Ap
18	440	11.6	334	US-11-072-512-2440	Sequence 2440, Ap
19	435	11.5	577	US-11-072-512-2569	Sequence 2569, Ap
20	434.5	11.5	1024	US-10-330-773-927	Sequence 927, App
21	433	11.4	575	US-11-072-512-3423	Sequence 3423, App
22	432.5	11.4	553	US-11-072-512-3306	Sequence 3306, Ap
23	432	11.4	816	US-11-072-512-2341	Sequence 2341, Ap
24	430.5	11.3	487	US-11-072-512-2868	Sequence 2868, Ap
25	428	11.3	407	US-11-072-512-3895	Sequence 3895, Ap

26	426.5	11.2	357	US-11-072-512-2570	Sequence 2570, Ap
27	425.5	11.2	526	US-11-072-512-3582	Sequence 3582, Ap
28	425.5	11.2	732	US-11-072-512-3474	Sequence 3474, Ap
29	424.5	11.2	350	US-11-072-512-2500	Sequence 2500, Ap
30	423.5	11.2	231	US-11-072-512-3821	Sequence 3821, Ap
31	423.5	11.2	462	US-11-072-512-3571	Sequence 3571, Ap
32	421.5	11.1	487	US-11-072-512-3083	Sequence 3083, Ap
33	421.5	11.1	498	US-11-072-512-2548	Sequence 2548, Ap
34	420	11.1	355	US-11-072-512-3671	Sequence 3671, Ap
35	419.5	11.1	437	US-11-072-512-2932	Sequence 2932, Ap
36	417.5	11.0	432	US-11-000-463-365	Sequence 365, App
37	415	10.9	720	US-11-121-438-2	Sequence 18, Appl1
38	410.5	10.8	689	US-11-121-438-2	Sequence 2, Appl1
39	409	10.8	445	US-11-072-512-2530	Sequence 2590, Ap
40	407.5	10.7	641	US-11-072-512-2385	Sequence 2385, Ap
41	406.5	10.7	1011	US-10-330-773-924	Sequence 924, App
42	405	10.7	494	US-11-072-175-181	Sequence 181, App
43	399.5	10.5	307	US-11-072-512-2986	Sequence 2986, Ap
44	399	10.5	302	US-11-072-512-2998	Sequence 2998, Ap
45	394	10.4	172	US-10-888-613B-75	Sequence 75, Appl

#### ALIGNMENTS

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RESULT 1
US-11-072-512-2929
; Sequence 2929, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OR INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2929
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
;
Query Match 13.3%, Score 503; DB 7; Length 799;
Best Local Similarity 24.3%; Pred. No. 5.7e-29;
Matches 186; Conservative 86; Mismatches 270; Indels 224; Gaps 32;
QY 33 DVTVIAREQFRKHTVIMACGLFYISFTDQKCNLSVINLDEINDEGCILLDFMYT 92
DB 27 DVAVAFREBEIR---LIDTQKRLRYDVMENFR-NIVAVGHLF-FQPD-----MV 72
QY 93 SKLWLRRESNIMAWMATMYLQMEHVVDTCRFEI-----KASEAEVNSAIK 137
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Db      73  SQAEMKMMETETORSSKQNKMETLOKFAKLYLNOGLSCWQIWMQVASELRLCQ 132
Qy      138  PRREEL-----NSRMLPDDIMAY-----RG 159
Db      133  GKSSQLQDSDSIQVSENENINMPKDDSIYLENOEPWRTQHSNGNTYLSQSQIQSG 192
Qy      160  REV-VENNLP-----LRSAFGCESSRAFAPLSVSGLSTPPASVSMYSHLVSSLFDEDF 213
Db      193  KQIDVANNIQLIHEDFMKSP-----FHEHKTDTPEPKCKGMEYK-----LISDGS- 239
Qy      214  RDVRFVAPNPFKERALPCDSAPVPEYSR-----PTEVSPNV-----C--HSNITS 260
Db      240  -NOKPLG-----EKHPHC-----GEGRGFSYSPRLPIHNVHTGKCFSGSSHRT 286
Qy      261  PKETIEBARSDMNVYVAGLKPAPASARN---APYPCDKASKBERPSSDEIALHAF 316
Db      287  HORIHGEKLMRCHBSGDCFNKSSFHSYOSNHTGKSYCDSCGKF---SSSTGLIHY 343
Qy      317  EPPNAPLNRKGLVSPSPKSDCQPNSPTEACSSKNACILQASGSPPAKSPTPDKACNMK 376
Db      344  RHTTG-----EKPYK-----CECGCKFSQS- 365
Qy      377  KYKFIYLSINQNAKPGGEQAEIG-----RLSPRAYTAPACOPMEBENLDQSPT 429
Db      366  --NFOGHQVHTEKPYKCECGKGFWSVNLVHQRVHRG-----EKPY 408
Qy      430  KLSASGSDSTIPQASRLNNTVNSMTGSPRSSB-----SH-SPLYMH-----PRK 474
Db      409  KCECGCKGFT--QAAHF-HIQRVHTGKPYKCDVCGKGFSSNSPLICHRRVHTGKPYK 465
Qy      475  CTSCGSQSPQAHMCLHTAGPTFAEMGETQSEYSSCENG----- 516
Db      466  CRAQCGKFTNTLHTH-----FRVHTG--KPYKCECGKGFSSQASNIQVHONVHTGK 518
Qy      517  AFPCNECDCFSEASIKRHTLQTHSDPKYCDRCOASFYKGNLASHTKVTHTGKPYK 576
Db      519  RPFCEFCGKGFSSKQLQTHQVHTGKPYKCDVCGKDFYSNLTQHVIHTGKPYK 578
Qy      577  NTCGAQPNRPANIKTTRIHSGEKPYKCECTCGARFQVQVLAHLVHTGKPYPELIG 636
Db      579  BECGKGFSSWSNLAHORVHSGEKPYKCEQCDKSFQALDFRVHORVHTGKPYKGVG 638
Qy      637  TRFRHQLTKSHLRHTGKPYKCEKCNLHFRHKSQRLRLRKHG 682
Db      639  KGFSSGSLQSHQVHTGKPYKCDVCGKGFYSQPIYHQHGTG 684

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## RESULT 2

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US-11-072-512-2161
; Sequence 2161, Application US/11072512
; Publication No. US2006029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191

```

```

; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2161
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2161

```

Query Match 12.4%; Score 469; DB 7; Length 541;

Best Local Similarity 28.6%; Pred. No. 1e-26; Matches 153; Conservative 60; Mismatches 188; Indels 134; Gaps 26;

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Qy      216  VMPPVNPFPKERALPCDSAPVPEYSRPTLEVPNVCHSNIVAPKETIPEARSDMHY 275
Db      3  LKQTTIRN-FP-BREVPD-----EVERFTREVP---CLSLGDMWDC--ENQGHILQ 49
Qy      276  SVABGLKPAAPARNAFYPCDKASKBERPSSDEIALHFPNPAPLNRKGLVSPQSQ 335
Db      50  SALTLEKEPQTORA-----ICEYPGFGRHLIASD-----LPPQRYLATNGFAPDENV 98
Qy      336  KS-DOQPSPT-----EACSSKNAC-----ILQASG---SPPAKSPTPDKACNM 375
Db      99  SGLDDCPALPSYPKSYADRTGSDACGKGFNSHMEVHGRNPNVREKPYKIPESVYKSFNH 158
Qy      376  -----KKYK-----FIVLSINQNAK--PGAPRO--AEIGR----- 402
Db      159  FTSLSGHQKIMRGKSKYEBKKNFENFTLSSSLNENQRMPLGKQYRCHTECGKCFRNSL 218
Qy      403  -LSPRAYTA--BPACOP--PMEBENLD-----QSPTLASG-----EDSTIPQAS 444
Db      219  VLHHRHTHTGKPYKCECGKSFSSKNVNLVHORVHTGKPYKCGKAFSDGSLTQHQ 278
Qy      445  RLNNIVNRSMTGSPRSSSSHSPLVMHPKCTSCGSQSPQAHMCLHTAGPTFAEMGET 504
Db      279  RHH-----TGE-----KPYECLECGTFNRNSLILHQHTHT-----GEK 313
Qy      505  QSEYSSCENGAFFPCNECDCFSEASIKRHTLQTHS-DKPYKCDRCOASFYKGNLAS 563
Db      314  -----PYCNBEGKRFDTLSLTVH-LAIHTGKPYECSKCGKARDDSYLQ 360
Qy      564  HKTVHTGKPYKCNICGAQPNRPANIKTTRIHSGEKPYKCECTCGARFQVQVLAHLV 623
Db      361  HERTHTGKPYFCACGKGFNSHSLIVHQKIHSGEKPYECKECCGKTFIESAYLIRHORI 420
Qy      624  HTGKPYPELIGTRFRHQLTKSHLRHTGKPYKCEKCNLHFRHKSQRLRLRKHG 678
Db      421  HTGKPYGNGOCOKLFRNTAGLIRHORIHTGKPYEKNQCGARFSDSCLTQHQR 475

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## RESULT 3

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US-11-072-512-3748
; Sequence 3748, Application US/11072512
; Publication No. US2006029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO

```



APPLICANT: SEKI, NAOHITO  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTOYUKI  
APPLICANT: NAGAHARI, KENJI  
APPLICANT: MASUHO, YASUHIKO  
TITLE OF INVENTION: Novel full length cDNA  
FILE REFERENCE: 084335-0191  
CURRENT APPLICATION NUMBER: US/11/072,512  
CURRENT FILING DATE: 2005-03-07  
PRIOR APPLICATION NUMBER: US 60/350,978  
PRIOR FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: JP 2001-379298  
PRIOR FILING DATE: 2001-11-05  
NUMBER OF SEQ ID NOS: 4096  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3748  
LENGTH: 540  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-072-512-3748

Query Match 12.4%; Score 468.5; DB 7; Length 540;  
Best Local Similarity 37.3%; Pred. No. 1,1e-26;  
Matches 91; Conservative 27; Mismatches 87; Indels 39; Gaps 4;

QY 472 PPKCTSCGSGSPQHAEMCLHT---AGPTFAEMGE--TQSE-----YSD 510  
DB 255 PYCEBCGKAFNPFNSLITTKIHTGBOPIYCECECKAFQSSSTLTTHRKIHTEKPYKC 314  
QY 511 SSGENG-----AFPCNCDRPSSEASLKRHITLQTHSDKPYKCDRCQ 552  
DB 315 BECGKAFNRSSKLTENKNIHTGBOPIYCECECKAFNRSNLTTHRKIHTEKPYKCEG 374  
QY 553 ASFRYGNLASHKTVHTGKPYRCNICGAQFNRPANLKTTHRIHSGEKPYKCECGARFV 612  
DB 375 KAKHSSALTTTHRKIHTEKPYKCECGKAFNRSSKLTENKNIHTGKPYKCECGARFV 434  
QY 613 QVAHLRAHVLHTGKPYPCIEIGTRFRHLQTLKSHLRIHTGKPYKCECNLHFRHSQ 672  
DB 435 QSSKLTENKNIHSGEIPYKCECGKAFKHSLSLTTHRKIHTEKPYKCECGKAFNRSSK 494

QY 673 LRLH 676  
DB 495 LTEH 498

RESULT 4  
US-11-072-512-2937  
Sequence 2937, Application US/11072512  
Publication No. US2006029945A1  
GENERAL INFORMATION:  
APPLICANT: ISOGAI, TAKAO  
APPLICANT: SUGIYAMA, TOMOYASU  
APPLICANT: OTSUKI, TETSUJI  
APPLICANT: WAKAMATSU, AI  
APPLICANT: SATO, HIROYUKI  
APPLICANT: ISHII, SHIZUKO  
APPLICANT: YAMAMOTO, JUN-ICHI  
APPLICANT: ISONO, YUUKO  
APPLICANT: HIO, YURI  
APPLICANT: OTSUKA, KAORU  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: IRIE, RYOTARO  
APPLICANT: TAMECHIKA, ICHIRO  
APPLICANT: SEKI, NAOHITO  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTOYUKI  
APPLICANT: NAGAHARI, KENJI  
APPLICANT: MASUHO, YASUHIKO  
TITLE OF INVENTION: Novel full length cDNA  
FILE REFERENCE: 084335-0191  
CURRENT APPLICATION NUMBER: US/11/072,512  
CURRENT FILING DATE: 2005-03-07

PRIOR APPLICATION NUMBER: US 60/350,978  
PRIOR FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: JP 2001-379298  
PRIOR FILING DATE: 2001-11-05  
NUMBER OF SEQ ID NOS: 4096  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2937  
LENGTH: 781  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-072-512-2937

Query Match 12.3%; Score 465.5; DB 7; Length 781;  
Best Local Similarity 38.4%; Pred. No. 2.9e-26;  
Matches 93; Conservative 29; Mismatches 91; Indels 29; Gaps 5;

QY 465 HSPLYMH-----PPKCTSCGSGSPQHAEMCLHT---AGPTFAEMGETQSYSDS 511  
DB 477 HSRLLAHQRHTGKPYKCNBCKGVFSQHSRLAVHRRIHTEKPYKCKEKGKV---FSDR 533  
QY 512 SC-----ENGAPFCNCDRPSSEASLKRHITLQTHSDKPYKCDRCQASFRYGNLA 562  
DB 534 SAFPARRRHITGKPYKCKEKGKRVFSQCSRLTVHRRIHSGEKPYKCNBCKGVFSQYSHLV 593  
QY 563 SHKTVHTGKPYRCNICGAQFNRPANLKTTHRIHSGEKPYKCECGARFVQVAHLRAHVL 622  
DB 594 GHRVHTGKPYKCECGKAFNPGSTLNHQRHTGKPYKCNQCNSTFSQVHLHLHOT 653  
QY 623 IHTGKPYPCIEIGTRFRHLQTLKSHLRIHTGKPYKCECNLHFRHSQ 678  
DB 654 VHTGDRPYKCNBCKGVFSQSNLTHQIHAQKPYKCECGKAFVHSSHLVSHQRIHTG 713  
QY 679 QK 680  
DB 714 EK 715

RESULT 5  
US-11-072-512-2592  
Sequence 2592, Application US/11072512  
Publication No. US2006029945A1  
GENERAL INFORMATION:  
APPLICANT: ISOGAI, TAKAO  
APPLICANT: SUGIYAMA, TOMOYASU  
APPLICANT: OTSUKI, TETSUJI  
APPLICANT: WAKAMATSU, AI  
APPLICANT: SATO, HIROYUKI  
APPLICANT: ISHII, SHIZUKO  
APPLICANT: YAMAMOTO, JUN-ICHI  
APPLICANT: ISONO, YUUKO  
APPLICANT: HIO, YURI  
APPLICANT: OTSUKA, KAORU  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: IRIE, RYOTARO  
APPLICANT: TAMECHIKA, ICHIRO  
APPLICANT: SEKI, NAOHITO  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTOYUKI  
APPLICANT: NAGAHARI, KENJI  
APPLICANT: MASUHO, YASUHIKO  
TITLE OF INVENTION: Novel full length cDNA  
FILE REFERENCE: 084335-0191  
CURRENT APPLICATION NUMBER: US/11/072,512  
CURRENT FILING DATE: 2005-03-07  
PRIOR APPLICATION NUMBER: US 60/350,978  
PRIOR FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: JP 2001-379298  
PRIOR FILING DATE: 2001-11-05  
NUMBER OF SEQ ID NOS: 4096  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2592  
LENGTH: 586  
TYPE: PRT

ORGANISM: Homo sapiens  
US-11-072-512-2592

Query Match 12.3%; Score 465; DB 7; Length 586;  
Best Local Similarity 37.8%; Pred. No. 2.2e-26;  
Matches 98; Conservative 31; Mismatches 106; Indels 24; Gaps 4;

QY 472 PKCTSCGSGSPDHMM-----CLHTA-GPTFAEMMB-----TSEYSDSCCENGAFFC 520  
DB 228 PYKCECGCAFNSSULTGKIIHTGKPYKCECGCAFNSSSTLTGKRIHTGKPYK 287  
QY 521 NECDGFSEASLKRHTLTQTHSDPKYCDRCQAFRYKGNLASHKTVHTGKPYRNCIG 580  
DB 288 EBCGKAFNQFSILNKHKRIHMDKPYKCECGCAFRVFSILKKHKIHTGKPYKCECG 347  
QY 581 AQPNRPANIKTRIRHSGKPYKCECGCAFRVQVLAHLRAVLIHTGKPYPCICGTRR 640  
DB 348 KAFNPSNLTGKRIHTGKPYKCECGCAFNOSSTLTGKRIHTGKPYKCECGCAFK 407  
QY 641 HQTLSKSHLRHTGKPYKCECGCAFNHFRKSQLRLRLRO-----KHGATWT 687  
DB 408 QSTLTREHKIHTGKPYKCECGCAFNSSAFTGKHKHMEDKPYKCECGCAFSVST 467  
QY 688 KQYRVASATDLPPELPKAC 706  
DB 468 LTKHKIHTREKPYKCEC 486

## RESULT 6

US-11-072-512-3914  
Sequence 3914, Application US/11072512  
Publication No. US20060029945A1  
GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO  
APPLICANT: SUGIYAMA, TOMOYASU  
APPLICANT: OTSUKI, TETSUJI  
APPLICANT: WAKAMATSU, AI  
APPLICANT: SATO, HIROYUKI  
APPLICANT: ISHII, SHIZUKO  
APPLICANT: YAMAMOTO, JUN-ICHI  
APPLICANT: HIO, YURI  
APPLICANT: OTSUKA, KAORU  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: IRIE, RYOTARO  
APPLICANT: TAMECHIKA, ICHIRO  
APPLICANT: SEKI, NAOHITO  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTOKYUKI  
APPLICANT: NAGAHARI, KENJI  
APPLICANT: MASUHO, YASUHIKO  
TITLE OF INVENTION: Novel full length cDNA  
FILE REFERENCE: 084335-0191  
CURRENT APPLICATION NUMBER: US/11/072,512  
CURRENT FILING DATE: 2005-03-07  
PRIOR APPLICATION NUMBER: US 60/350,978  
PRIOR FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: JP 2001-379298  
PRIOR FILING DATE: 2001-11-05  
NUMBER OF SEQ ID NOS: 4096  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3914  
LENGTH: 586  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-072-512-3914

Query Match 12.2%; Score 463; DB 7; Length 556;  
Best Local Similarity 26.7%; Pred. No. 2.9e-26;  
Matches 156; Conservative 76; Mismatches 218; Indels 134; Gaps 22;  
QY 147 RMLPQDIAVYRREVENN-LPLR-----SAPGCSRAFAFSLYSGLTTPPASYSMYSH 200

DB 42 RVIVPVLGHRNPVARDASAVPARAPMLQEDKVEERANAPGLPTACOSQBPVTFAV-- 99  
QY 201 LPVSLLESDER-----PRDVM-----PYANFPKRALPCOSARVPGEY 242  
DB 100 ---AVVTFPEBWFLDSTQSLYHDVNLRYNLASVADOLCKNALSTYLEER---GEQ 152  
QY 243 SRPTLEVPNVCHSNIVSPKETIPEARSMDHYV-ABGLPRAAPSARNAPFPCKASK 301  
DB 153 WTRDGVLDPCABRQCQPGALPQDFTTEILSDVXGEQO-----PEKLYK 202  
QY 302 --EERPSSEEDIALHFPNPAPLNRKGLVSPQSKDCCPNSTFACSSGNACILQAS 359  
DB 203 YNELEKPPNLSIEPLRQYRIHA-----GASCEQ-----EIRNSFFQSAH 243  
QY 360 GSPPAKSPDPK--ACNKKYKFIVLNGLNAPKPGEGA---ELG-----RLS 404  
DB 244 LIVPEKISGDKSYACNCKEFSRYSSDLIRHEKHTHEKCDQCECGCAFRYSNLRH 303  
QY 405 PRAYTAPRACOPMPEBNIDLQSPYKLSASGEDSTIPQASRLNIV--NRSMTGPRSSS 462  
DB 304 MTHTG-----EKPECGCGKFT-----RNFNLILHQRNHTG----- 338  
QY 463 BSHSPLVHAPPKCTSCGSGSPDHMMCLHTAGPTFAEMGETQSEYSDSCCENGAFFCNE 522  
DB 339 -----KPYECKDCGCAFNQPSLSRSHVTRHT-----GEK-----DFECGQ 373  
QY 523 CDCRPFSEASLKRHTLTQTHS--DKPYCDRCQAFRYKGNLASHKTVHTGKPYRNCIGA 581  
DB 374 CKAIFREHSSLTTH--LRHTTREKPYECNOCGKPFRTSHLNVKRIHTGKLYEACATCQ 432  
QY 582 QPNRPANIKTRIRHSGKPYKCECGCAFRVQVLAHLRAVLIHTGKPYPCICGTRR 641  
DB 433 VLSRLSTLSKSHRHTGKPYKCECGCAFRVPSLSRKHARTSHKGYACGCGCARAQ 492  
QY 642 LQTLKSHLRHTGKPYKCECGCAFNHFRKSQLRLRLROKHAIT 685  
DB 493 SSSLIVVYVTHSAGRPOCNCCEKAFRHSSTLTGKRIHTGRET 536

## RESULT 7

US-11-072-512-2805  
Sequence 2805, Application US/11072512  
Publication No. US20060029945A1  
GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO  
APPLICANT: SUGIYAMA, TOMOYASU  
APPLICANT: OTSUKI, TETSUJI  
APPLICANT: WAKAMATSU, AI  
APPLICANT: SATO, HIROYUKI  
APPLICANT: ISHII, SHIZUKO  
APPLICANT: YAMAMOTO, JUN-ICHI  
APPLICANT: ISONO, YUUKO  
APPLICANT: HIO, YURI  
APPLICANT: OTSUKA, KAORU  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: IRIE, RYOTARO  
APPLICANT: TAMECHIKA, ICHIRO  
APPLICANT: SEKI, NAOHITO  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTOKYUKI  
APPLICANT: NAGAHARI, KENJI  
APPLICANT: MASUHO, YASUHIKO  
TITLE OF INVENTION: Novel full length cDNA  
FILE REFERENCE: 084335-0191  
CURRENT APPLICATION NUMBER: US/11/072,512  
CURRENT FILING DATE: 2005-03-07  
PRIOR APPLICATION NUMBER: US 60/350,978  
PRIOR FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: JP 2001-379298  
PRIOR FILING DATE: 2001-11-05  
NUMBER OF SEQ ID NOS: 4096  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2805

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; LENGTH: 561
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2805

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Query Match	12.1%;	Score 458.5;	DB 7;	Length 561;
Best Local Similarity.	30.6%;	Pred. No. 6.3e-26;		
Matches 138;	Conservative 47;	Mismatches 167;	Indels 99;	Gaps 18;

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:
: NUMBER OF SEQ ID NOS: 4096
:
: SOFTWARE: Patentin Ver. 2.1
:
: SEQ ID NO 3434
:
: LENGTH: 530
:
: TYPE: PRY
:
: ORGANISM: Homo sapiens
:
: US-11-072-512-3434

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Query Match	12.1%;	Score 458;	DB 7;	Length 530;
Best Local Similarity	39.0%;	Pred. No. 6.4e-26;		
Matches 94;	Conservative 27;	Mismatches 88;	Indels 32;	Gaps 4;

[illegible]

```

QY      444  SRLNIV--NRSMGSPRSESHSLPLYMHPKICSCGSGPQHAENCLHTGPTFAEEM 500
      ||:::  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      308  SRMSVTLLMRSHITGE-----KPYCKNCKGKAPSQCSVFIIHMRSHT----- 349

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409 TAPPAC-----PPME-----PEN-----LDLQSPTKLSASG 435

Dy 502 GETQSEYSDSSCENGAFPCBCDCDFRSREASLNKRLLTLCIDHNAFICLDRCCQSFRINAD 50

| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |

Db 350 GEK-----PYVCECGKAFFSQSSLTVHNRNHTAEKPYEKECKGKAFSRKENT 397

Dy 436 EDSITIPQASRLNNIVNRSMTGSPRRSSBSHSPPLMH-----PFCISCG--SOS 48

Db 229 NLPIQIRHSINNIIETNECGTFSEK----LVLHLQORTHTGEXPDYECHECGKTFPOK 283

398 ITHOKIHTBEKPYECSECCGAFIOMNSNLHQRHTHGEKPYACTVCGKAFSQKSNLITEB 45

Db 284 SAHTRHQRHTGKRYECHECGKTFYKNSDLIKQRIHTGERPYGCHGCGKSFSEKSTLT 343

Db 458 KIHTEKPHCNQCKAFSGRQNLLEHKIHTGEKFPKCNCKGKAFSRISLTILHVRSH 517

DB 344 QHQ-RTHGGEKPYECHECGKTFSPKSVLTVHQKTHGGEKPYECYACGKAFLRKSDLIHQ 40

Db 518 G 518

Db 403 RIHTGEKPYECNECGSKSFSEKSTLYTKHLRHTGEKPYECIQCGKFFCYYSGFTEHLRHTT 46

US-11-072-512-2663  
; Sequence 2663, Application US/11072512  
; Publication No. US20060029945A1

Db 463 GEKPFGCNECGKTFROKSALIVHÖRTHIRÖK 493

; APPLICANT: ISOGAI, TAKAO  
 ;  
 ; APPLICANT: SUGIYAMA, TOMOYASU  
 ;  
 ; APPLICANT: OTSUKI, TETSUI  
 ;  
 ; APPLICANT: WAKAMATSU, AI

US-11-072-512-3434  
; Sequence 3434, Application US/11072512  
; Publication No. US20060029945A1

```

; APPLICANT: SAITO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUTKO

```

;  
 ; APPLICANT: ISOGAI, TAKAO  
 ;  
 ; APPLICANT: SUGIYAMA, TOMOYASU  
 ;  
 ; APPLICANT: OTSUKI, TETSUJI

/ THE FILE CONTAINS:  
 / APPLICANT: OTSUKA, KAORU  
 / APPLICANT: NAGAI, KEIICHI  
 / APPLICANT: IRIE, RYOTARO  
 / APPLICANT: MATSUYAMA, TOSHIO

1  
/  
APPLICANT:  
/  
APPLICANT:  
/  
APPLICANT:  
/

CHIEF, MIKAZUKI  
ISHII, SHIZUKO  
YAMAMOTO, JUN-ICHI  
MIKAZUKI, YUKIO

APPLICANT: SEKI, NAOHICO  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTUYUKI  
APPLICANT: NAGAHARI, KENJI

```

; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO

```

```

; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 08435-0191
; CURRENT APPLICATION NUMBER: US/11/072,512

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```

; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI

```

PRIOR APPLICATION NUMBER: US 60/350,978  
PRIOR FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: JP 2001-379298

```

1  REFERENCE: 145820; 1100-1101
2  TITLE OF INVENTION: Novel full length cDNA
3  FILE REFERENCE: 084335-0191
4  COUNTRY AND INVENTOR NUMBER: US/11/072 512

```

```

; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2663
; LENGTH: 409

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; PRIOR APPLICATION NUMBER: US 60/350,978  
 ; PRIOR FILING DATE: 2002-01-25  
 ; PRIOR APPLICATION NUMBER: JP 2001-379298

```

; LIFE: FRI
; ORGANISM: Homo sapiens
US-11-072-512-2663

```

Best Local Similarity 36.2%; Pred. No. 5.5e-26;  
Matches 93; Conservative 25; Mismatches 91; Indels 48; Gaps 4.

[illegible]

RESULT 10  
US-11-072-512-3470

```

1  APPLICANT: ISOGAI, TAKAO
2  APPLICANT: SUGIYAMA, TOMOYASU
3  APPLICANT: OTSUKI, TETSUJI
4  APPLICANT: MAKAMATSU, AI
5  APPLICANT: SATO, HIROYUKI
6  APPLICANT: ISHII, SHIZUKO
7  APPLICANT: YAMAMOTO, JUN-ICHI
8  APPLICANT: ISONO, YUUKO
9  APPLICANT: HIO, YURI
10 APPLICANT: OTSUKA, KAORU
11 APPLICANT: NAGAI, KEIICHI
12 APPLICANT: IRIE, RYOTARO
13 APPLICANT: TAMECHIKA, ICHIRO
14 APPLICANT: SEKI, NAOHIKO
15 APPLICANT: YOSHIKAWA, TSUTOMU
16 APPLICANT: OTSUKA, MOTOTYUKI
17 APPLICANT: NAGAHARI, KENJI
18 APPLICANT: MASUHO, YASUHIKO
19 TITLE OF INVENTION: Novel full length cDNA
20 FILE REFERENCE: 084335-0191
21 CURRENT APPLICATION NUMBER: US/11/072,512
22 CURRENT FILING DATE: 2005-03-07
23 PRIOR APPLICATION NUMBER: US 60/350,978
24 PRIOR FILING DATE: 2002-01-25
25 PRIOR APPLICATION NUMBER: JP 2001-379298
26 PRIOR FILING DATE: 2001-11-05
27 NUMBER OF SEQ ID NOS: 4096
28 SOFTWARE: PatentIn Ver. 2.1
29 SEQ ID NO 3470
30 LENGTH: 475
31 TYPE: PRT
32 ORGANISM: Homo sapiens
33 US-11-072-512-3470

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Query Match Similarity      12.0% ; Score 457; DB 7; Length 475;  
Best Local Similarity    36.2%; Pred No. 6,6e-26;  
Matches     93; Conservative   25; Mismatches   91; Indels   48; Gaps   4  
  
QY       461 SSESHPLYM-----HPPKCTSGCGSOPDAEMCLHTAGPTEAEEM 501  
          :|::|||:||||:  
Db        139 SEEIFTPPEWPFIIQTPLTLHQINNEDRPYECKKGAFASGNSQFIQH----QR I 191  
          |||||  
QY       502 GTGTSEBYSDSCENGAF-----CNECDRPSFEASLKRPTLTQTH 541  
          ::::::|:
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Db	192	HIGKSYECKEC--GKPFSCSHYTRHLKHTGKRPCEKCGKAFSCSSYLSDHQHRT	249
Qy	542	SDRPYKCDRCQASFRYKGNLASHKTVHTGEKPRYCNICGAOFNRPANULKTHTRIHSEKPR	601
Db	250	GKRPYCEKCGKAFSCSYNSLIDHQRIHTGKRPYEKTCVGKAFYTSQSLFOHARIHTGEKP	309
Qy	602	YKRETCGAFVQVANHRAVLHTGKEKYPPEIGSTRPHRLQTLKSHLRHTGKEKPYNCE	661
Db	310	YEKEGKGAFTSSKYLQHQRIHTGEKPYECKGKAFSSGSLALNHQRIHTGKEKPYDCK	369
Qy	662	KNLHPFHKSQSLRLHLR	678
Db	370	ECGKAFYSSQLRQHQH	386

RESULT 11  
US-11-072-512-2786  
; Sequence 2786, Application US/11072512  
; Publication No. US20060029945A1  
; GENERAL INFORMATION:

```

/ APPLICANT: ISOGAI, TAKAO
/ APPLICANT: SUGIYAMA, TOMOYASU
/ APPLICANT: OTSUKI, TETSUJI
/ APPLICANT: WAKAMATSU, AI
/ APPLICANT: SATO, HIROYUKI
/ APPLICANT: ISHII, SHIZUKO
/ APPLICANT: YAMAMOTO, JUN-ICHI
/ APPLICANT: ISONO, YUTUKO
/ APPLICANT: HIO, YURI
/ APPLICANT: OTSUKA, KAORU
/ APPLICANT: NAGAI, KEIICHI
/ APPLICANT: IRIE, RYOTARO
/ APPLICANT: TAMECHIKA, ICHIRO
/ APPLICANT: SEKI, NAORIKO
/ APPLICANT: YOSHIKAWA, TSUTOMU
/ APPLICANT: OTSUKA, MOTOKU
/ APPLICANT: NAGAHARI, KENJI
/ APPLICANT: MASUHO, YASUHIKO
/ TITLE OF INVENTION: Novel full length cDNA
/ FILE REFERENCE: 084335-0191
/ CURRENT APPLICATION NUMBER: US/11/072,512
/ PRIOR FILING DATE: 2005-03-07
/ PRIOR APPLICATION NUMBER: US 60/350,978
/ PRIOR FILING DATE: 2002-01-25
/ PRIOR APPLICATION NUMBER: JP 2001-379238
/ PRIOR FILING DATE: 2001-11-05
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2786
/ LENGTH: 429
/ TYPE: prt
/ ORGANISM: Homo sapiens
/ US-11-072-512-2786

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Query Match	12.0%;	Score 455;	DB 7;	Length 429;
Best Local Similarity	34.9%;	Pred. NO. 8.2e-26;		
Matches 104; Conservative	40;	Mismatches 131;	Indels 23;	Gaps 7

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QY 421 EULDIOSPKLASGSDSTIPQASRLN--NIVRWSTGSPRSSSESHSPLYMHPKPTGSC 478
Db 123 EKLANKMPEFGVITYBEKLTIPGGESEKKNNDGNSLTVAWSNLISHQRLPVGDRPHKDEC 188
QY 479 GSQSPDHAEMC---LHTAGTPFAEBMGSTGSEYSDS-----CENGAFPCNECDC 525
Db 189 SKSPFRTSDLIHQHRIHTEKPEY--ECNECGKAFSSSHLIQHORIHTEKPEYECSDCGK 246
QY 526 RSESEASLKRHTLQTHSDPKYCDKQASFRKGNLASHKTYHTEKPEYRCNICGAQFNR 585
Db 247 TFCSSSALIHRIHTEKPEYECNECGKFTWSSTLTHQRIHTEKPAVCNCGKAFSR 306
QY 586 PANKLTHTRIHSGEKPKYCKETGARGVQVAH.RAVLIHTEKPEYCEICGTRFRHLQTL 645
Db 307 SSTLIHHQRIHTEKPEYECNECGKAFSSSHLIQHORIHTEKPEYECNECGKFTYISGL 366

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OM protein - protein search, using sw model

Run on: March 2, 2006, 04:05:02 ; Search time 167 Seconds  
(without alignments)  
1766.392 Million cell updates/sec

Title: US-10-755-889-18

Sequence: 1 MASPADSCIOFTRHSDVLL.....TKYQVRVSATDLPPELPKAC 706

Scoring table: BLOSUM62  
Gapco 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications\_AA\_Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3793	100.0	706	US-10-755-889-18	Sequence 18, Appl
2	3777	99.6	706	US-10-755-889-66	Sequence 66, Appl
3	3771	99.4	706	US-10-408-765A-1988	Sequence 1988, Ap
4	3763	99.2	706	US-09-107-058-2	Sequence 2, Appl
5	3763	99.2	706	US-09-761-117-2	Sequence 16, Appl
6	1155	30.5	479	US-10-295-027-16	Sequence 24, Appl
7	1155	30.5	479	US-10-211-462-24	Sequence 24, Appl
8	1122.5	29.6	518	US-09-815-379-4	Sequence 4, Appl
9	618.5	16.3	810	US-10-974-470-27	Sequence 21, Appl
10	610	16.1	803	US-10-441-854-9	Sequence 9, Appl
11	564.5	14.9	765	US-10-486-977-12	Sequence 12, Appl
12	560	14.8	110	US-09-107-058-9	Sequence 9, Appl
13	560	14.8	110	US-09-761-117-9	Sequence 9, Appl
14	552	14.6	108	US-10-164-359-3	Sequence 3, Appl
15	540	13.8	688	US-10-477-646-21	Sequence 21, Appl
16	522.5	13.2	610	US-10-221-625-10	Sequence 10, Appl
17	517	13.6	711	US-10-034-934-90	Sequence 90, Appl
18	504	13.3	678	US-10-296-115-1316	Sequence 1316, Ap
19	503	13.3	799	US-10-104-047-2929	Sequence 2929, Ap
20	501	13.2	673	US-10-756-149-4775	Sequence 4775, Ap
21	501	13.2	819	US-10-108-260A-3302	Sequence 3302, Ap
22	497.5	13.1	1050	US-10-450-763-40044	Sequence 40044, A
23	497	13.1	458	US-10-408-765A-2340	Sequence 2340, Ap
24	495.5	13.1	638	US-10-723-860-1613	Sequence 1613, Ap
25	494.5	13.0	597	US-10-136-728-58	Sequence 58, Appl
26	494	13.0	595	US-10-203-052B-8	Sequence 8, Appl
27	492	13.0	1520	US-10-450-763-57489	Sequence 57489, A

28	490.5	12.9	606	US-10-074-978A-117	Sequence 117, App
29	489	12.9	340	US-10-450-763-35320	Sequence 35320, A
30	488.5	12.9	587	US-10-029-386-32268	Sequence 32268, A
31	488	12.9	464	US-10-108-260A-3590	Sequence 3590, Ap
32	486.5	12.8	577	US-10-381-327-3	Sequence 3, Appl
33	486.5	12.8	613	US-10-408-765A-1517	Sequence 1517, Ap
34	485.5	12.8	498	US-10-094-749-1657	Sequence 1657, Ap
35	485.5	12.8	517	US-10-450-763-33734	Sequence 33734, A
36	485	12.8	832	US-10-450-763-40902	Sequence 40902, A
37	483.5	12.7	406	US-09-764-864-976	Sequence 976, App
38	483	12.7	458	US-10-719-993-448	Sequence 448, App
39	483	12.7	458	US-10-719-993-449	Sequence 449, App
40	483	12.7	488	US-09-840-787-17	Sequence 17, Appl
41	483	12.7	803	US-10-408-765A-1049	Sequence 1049, Ap
42	479	12.6	632	US-10-450-763-48745	Sequence 48745, A
43	477	12.6	540	US-10-029-386-32805	Sequence 32805, A
44	476.5	12.6	697	US-10-408-765A-2256	Sequence 2256, Ap
45	476.5	12.6	697	US-10-723-860-4408	Sequence 4408, Ap

ALIGNMENTS

RESULT 1									
US-10-755-889-18									
Sequence 18, Application US/10755889									
Publication No. US20040171823A1									
GENERAL INFORMATION:									
APPLICANT: Bristol-Myers Squibb Company									
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB									
TITLE OF INVENTION: PATHWAY									
FILE REFERENCE: D0284 NP									
CURRENT APPLICATION NUMBER: US/10/755,889									
CURRENT FILING DATE: 2004-01-13									
PRIOR APPLICATION NUMBER: U.S. 60/440,068									
PRIOR FILING DATE: 2003-01-14									
PRIOR APPLICATION NUMBER: U.S. 60/469,757									
PRIOR FILING DATE: 2003-05-12									
NUMBER OF SEQ ID NOS: 823									
SOFTWARE: PatentIn version 3.2									
SEQ ID NO 18									
LENGTH: 706									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-10-755-889-18									
Query Match									
Best Local Similarity 100.0%; Score 3793; DB 4; Length 706;									
Best Local Similarity 100.0%; Pred. No. 6.6e-240;									
Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	MASPADSCIOFTRHSDVLLINLRSDILITDVIVVSRBQFRAKTVLMACGLFYSI	60						
Db	1	MASPADSCIOFTRHSDVLLINLRSDILITDVIVVSRBQFRAKTVLMACGLFYSI	60						
Qy	61	FTDOLKKNLSVINLDEINDEGFCILLDFMTSLNLRGINVAMATAMYLQHEHYVDI	120						
Db	61	FTDOLKKNLSVINLDEINDEGFCILLDFMTSLNLRGINVAMATAMYLQHEHYVDI	120						
Qy	121	CRKRTKSEAMYSAPKPRPEEFNLSHMLPQDIMAAYRGVEVNNLPLNSAPCESRAF	180						
Db	121	CRKRTKSEAMYSAPKPRPEEFNLSHMLPQDIMAAYRGVEVNNLPLNSAPCESRAF	180						
Qy	121	CRKRTKSEAMYSAPKPRPEEFNLSHMLPQDIMAAYRGVEVNNLPLNSAPCESRAF	180						
Db	121	CRKRTKSEAMYSAPKPRPEEFNLSHMLPQDIMAAYRGVEVNNLPLNSAPCESRAF	180						
Qy	181	APSLYSGISTPPASYSWYSHLPVSSLLPSDEEFDVMPVAPNPCKERAPPCDSARPYRG	240						
Db	181	APSLYSGISTPPASYSWYSHLPVSSLLPSDEEFDVMPVAPNPCKERAPPCDSARPYRG	240						
Qy	241	EYSRPTLEVSPNCHSNIVSPKETTPEEASDMHYVAEGLKPAAPARNAFYPCCKAS	300						
Db	241	EYSRPTLEVSPNCHSNIVSPKETTPEEASDMHYVAEGLKPAAPARNAFYPCCKAS	300						
Qy	301	KEERPSSEDEIALHFPFPNAPLNKGLVSPQSPKSDCOPNPTPEACSSKNACITLQASG	360						
Db	301	KEERPSSEDEIALHFPFPNAPLNKGLVSPQSPKSDCOPNPTPEACSSKNACITLQASG	360						

QY 361 SPPAKSPDTPKACNMKKYFIVLNSLNQNAKPGPQAEIGRLSPRAYTAPACOPMPMP 420  
 DB 361 SPPAKSPDTPKACNMKKYFIVLNSLNQNAKPGPQAEIGRLSPRAYTAPACOPMPMP 420  
 QY 421 ENLDIOSPTKLASGSDSTTPQASRLNNTVNSMTGSPRSSSESHSPLYMHPKCTSCGS 480  
 DB 421 ENLDIOSPTKLASGSDSTTPQASRLNNTVNSMTGSPRSSSESHSPLYMHPKCTSCGS 480  
 QY 481 OSPQHAEMCLHTAGPTFAEEMGETQSEYSDSCENGAFFCNECDRCFSEBASLKHHTLOT 540  
 DB 481 OSPQHAEMCLHTAGPTFAEEMGETQSEYSDSCENGAFFCNECDRCFSEBASLKHHTLOT 540  
 QY 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYPCNICGAQFNNRPAULKHTTRJHSGBK 600  
 DB 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYPCNICGAQFNNRPAULKHTTRJHSGBK 600  
 QY 601 PYKCECTGARFVQVAHLRAHVLHTGKPYPCNICGAQFNNRPAULKHTTRJHSGBK 660  
 DB 601 PYKCECTGARFVQVAHLRAHVLHTGKPYPCNICGAQFNNRPAULKHTTRJHSGBK 660  
 QY 661 EKCNIHFRHKSQRLRLRQKHGALINTKYQYVSATDLPPELPKAC 706  
 DB 661 EKCNIHFRHKSQRLRLRQKHGALINTKYQYVSATDLPPELPKAC 706

## RESULT 2

US-10-755-889-66  
 ; Sequence 66, Application US/10755889  
 ; Publication No. US20040171823A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB  
 ; FILE REFERENCE: D0284 NP  
 ; CURRENT APPLICATION NUMBER: US/10/755,889  
 ; CURRENT FILING DATE: 2004-01-13  
 ; PRIOR APPLICATION NUMBER: U.S. 60/440,068  
 ; PRIOR FILING DATE: 2003-01-14  
 ; PRIOR APPLICATION NUMBER: U.S. 60/469,757  
 ; PRIOR FILING DATE: 2003-05-12  
 ; NUMBER OF SEQ ID NOS: 823  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 66  
 ; LENGTH: 706  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-755-889-66

Query Match 99.6%; Score 3777; DB 4; Length 706;  
 Best Local Similarity 99.6%; Pred. No. 7.4e-239;  
 Matches 703; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MASPADSCIOFTRHASDVLNLRNLSRDILTDVIVVSRQFRAKTVLMACSGIFYSI 60  
 DB 1 MASPADSCIOFTRHASDVLNLRNLSRDILTDVIVVSRQFRAKTVLMACSGIFYSI 60  
 QY 61 FTDLKCNLSVINLDEINDEGFCILLDFMTSRNLREGNIMAVATAMYLQMEHVDT 120  
 DB 61 FTDLKCNLSVINLDEINDEGFCILLDFMTSRNLREGNIMAVATAMYLQMEHVDT 120  
 QY 121 CRKFTKASAEWVAIKPREEFILNSRMLMPODIMAYRGREVENNLPLRSAPGCSRAAF 180  
 DB 121 CRKFTKASAEWVAIKPREEFILNSRMLMPODIMAYRGREVENNLPLRSAPGCSRAAF 180  
 QY 181 APSLYSGLSTPPASYSMTSLPVSSLLFSDDEFRDVMPVAMPFKERALPCDSAPVPVG 240  
 DB 181 APSLYSGLSTPPASYSMTSLPVSSLLFSDDEFRDVMPVAMPFKERALPCDSAPVPVG 240  
 QY 241 EYSRPTLEVPVNCNSNITVPKETTIPERASDMHYSVABGLKPAAPBARNAFYFPCDKAS 300  
 DB 241 EYSRPTLEVPVNCNSNITVPKETTIPERASDMHYSVABGLKPAAPBARNAFYFPCDKAS 300

QY 301 KEERSSSEDEIALHFEPNAPLNRKGLVSPQSPKSDCCQNSPTEACSSKNACILQASG 360  
 DB 301 KEERSSSEDEIALHFEPNAPLNRKGLVSPQSPKSDCCQNSPTEACSSKNACILQASG 360  
 QY 361 SPPAKSPDTPKACNMKKYFIVLNSLNQNAKPGPQAEIGRLSPRAYTAPACOPMPMP 420  
 DB 361 SPPAKSPDTPKACNMKKYFIVLNSLNQNAKPGPQAEIGRLSPRAYTAPACOPMPMP 420  
 QY 421 ENLDIOSPTKLASGSDSTTPQASRLNNTVNSMTGSPRSSSESHSPLYMHPKCTSCGS 480  
 DB 421 ENLDIOSPTKLASGSDSTTPQASRLNNTVNSMTGSPRSSSESHSPLYMHPKCTSCGS 480  
 QY 481 OSPQHAEMCLHTAGPTFAEEMGETQSEYSDSCENGAFFCNECDRCFSEBASLKHHTLOT 540  
 DB 481 OSPQHAEMCLHTAGPTFAEEMGETQSEYSDSCENGAFFCNECDRCFSEBASLKHHTLOT 540  
 QY 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYPCNICGAQFNNRPAULKHTTRJHSGBK 600  
 DB 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYPCNICGAQFNNRPAULKHTTRJHSGBK 600  
 QY 601 PYKCECTGARFVQVAHLRAHVLHTGKPYPCNICGAQFNNRPAULKHTTRJHSGBK 660  
 DB 601 PYKCECTGARFVQVAHLRAHVLHTGKPYPCNICGAQFNNRPAULKHTTRJHSGBK 660  
 QY 661 EKCNIHFRHKSQRLRLRQKHGALINTKYQYVSATDLPPELPKAC 706  
 DB 661 EKCNIHFRHKSQRLRLRQKHGALINTKYQYVSATDLPPELPKAC 706

## RESULT 3

US-10-408-765A-1988  
 ; Sequence 1988, Application US/10408765A  
 ; Publication No. US20040101874A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; APPLICANT: Fahy, Boia D.  
 ; APPLICANT: Zhang, Bing  
 ; APPLICANT: Gibson, Bradford W.  
 ; APPLICANT: Taylor, Steven W.  
 ; APPLICANT: Glenn, Gary M.  
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
 ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
 ; FILE REFERENCE: 660088, 465  
 ; CURRENT APPLICATION NUMBER: US/10/408,765A  
 ; CURRENT FILING DATE: 2003-04-04  
 ; NUMBER OF SEQ ID NOS: 3077  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1988  
 ; LENGTH: 706  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-408-765A-1988

Query Match 99.4%; Score 3771; DB 4; Length 706;  
 Best Local Similarity 99.4%; Pred. No. 1.8e-238;  
 Matches 702; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MASPADSCIOFTRHASDVLNLRNLSRDILTDVIVVSRQFRAKTVLMACSGIFYSI 60  
 DB 1 MASPADSCIOFTRHASDVLNLRNLSRDILTDVIVVSRQFRAKTVLMACSGIFYSI 60  
 QY 61 FTDLKCNLSVINLDEINDEGFCILLDFMTSRNLREGNIMAVATAMYLQMEHVDT 120  
 DB 61 FTDLKCNLSVINLDEINDEGFCILLDFMTSRNLREGNIMAVATAMYLQMEHVDT 120  
 QY 121 CRKFTKASAEWVAIKPREEFILNSRMLMPODIMAYRGREVENNLPLRSAPGCSRAAF 180  
 DB 121 CRKFTKASAEWVAIKPREEFILNSRMLMPODIMAYRGREVENNLPLRSAPGCSRAAF 180  
 QY 181 APSLYSGLSTPPASYSMTSLPVSSLLFSDDEFRDVMPVAMPFKERALPCDSAPVPVG 240  
 DB 181 APSLYSGLSTPPASYSMTSLPVSSLLFSDDEFRDVMPVAMPFKERALPCDSAPVPVG 240



QY 241 EYGRPTLEVPNVCHSNISYPKETIPEARS DMHYSVAEGLKPAAPARNAFYPCDKAS 300  
 DB 241 EYGRPTLEVPNVCHSNISYPKETIPEARS DMHYSVAEGLKPAAPARNAFYPCDKAS 300  
 QY 301 KEERPESSDEIALHFEPPNAPLNKGLVSPQSPKSDCCPNSTPTEACSSKNACILQASG 360  
 DB 301 KEERPESSDEIALHFEPPNAPLNKGLVSPQSPKSDCCPNSTPTEACSSKNACILQASG 360  
 QY 361 SPPAKSPTDPKACMCKKXKFIIVNSLQNAKPGPEQAEIGRLSPRAYTAPPAQOPMPEP 420  
 DB 361 SPPAKSPTDPKACMCKKXKFIIVNSLQNAKPGPEQAEIGRLSPRAYTAPPAQOPMPEP 420  
 QY 421 ENLDOSPTKLSASGEDSTIPOASRLNNIYNRSMTGSPRSSSHSPLYNHMPKCTSCGS 480  
 DB 421 ENLDOSPTKLSASGEDSTIPOASRLNNIYNRSMTGSPRSSSHSPLYNHMPKCTSCGS 480  
 QY 481 QSPQHAMCMTHTAGPTAEEMGETQSEYSDSSCENGAFCNECDRCRSEASLKRHTLOT 540  
 DB 481 QSPQHAMCMTHTAGPTAEEMGETQSEYSDSSCENGAFCNECDRCRSEASLKRHTLOT 540  
 QY 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTEKPYPCICGTRFRHLQTLKSHLRHTGEKPYHC 600  
 DB 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTEKPYPCICGTRFRHLQTLKSHLRHTGEKPYHC 600  
 QY 601 PYKCTCGARFVOVAHLRAVHLIHTGEKPYPCICGTRFRHLQTLKSHLRHTGEKPYHC 660  
 DB 601 PYKCTCGARFVOVAHLRAVHLIHTGEKPYPCICGTRFRHLQTLKSHLRHTGEKPYHC 660  
 QY 661 EKNLHFRHKSQRLRLHROKGAITNTKQVRYVSATDLPPELPRAC 706  
 DB 661 EKNLHFRHKSQRLRLHROKGAITNTKQVRYVSATDLPPELPRAC 706

RESULT 4  
 US-09-107-058-2  
 Sequence 2, Application US/09107058  
 Patent No. US20010010922A1  
 GENERAL INFORMATION:  
 APPLICANT: Dalla-Favera, Riccardo  
 APPLICANT: Niu, Hui-Peng  
 TITLE OF INVENTION: CLONING AND USES OF THE GENETIC  
 TITLE OF INVENTION: LOCUS bcl-6  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/107,058  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 278-0400  
 TELEFAX: (212) 391-0525  
 TELEX: 422523 COOP UI  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 706 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-09-107-058-2  
 Query Match 99.3%; Score 3763; DB 3; Length 706;  
 Best Local Similarity 99.3%; Pred. No. 6,1e-238;  
 Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MASPASCTQFTHASDVLTNRLSRDLITGVIVSREQRAKTVLMAGSGFYSI 60  
 DB 1 MASPASCTQFTHASDVLTNRLSRDLITGVIVSREQRAKTVLMAGSGFYSI 60  
 QY 61 FTDLKCNLSVINLDEINEBEGCIILDFMYTSRLNLRGINAVATAMVTLQMEHVDT 120  
 DB 61 FTDLKCNLSVINLDEINEBEGCIILDFMYTSRLNLRGINAVATAMVTLQMEHVDT 120  
 QY 121 CRFTKASEAMVSAIKPREEFLNSRMTPQDIMA YRGREVENNMLPLASAGCESRAF 180  
 DB 121 CRFTKASEAMVSAIKPREEFLNSRMTPQDIMA YRGREVENNMLPLASAGCESRAF 180  
 QY 181 APSLYSGLSSTPPASYSMTSHLPVSSLLFSDDEFRDVMVPANPPKERALPCDSARVPV 240  
 DB 181 APSLYSGLSSTPPASYSMTSHLPVSSLLFSDDEFRDVMVPANPPKERALPCDSARVPV 240  
 QY 241 EYGRPTLEVPNVCHSNISYPKETIPEARS DMHYSVAEGLKPAAPARNAFYPCDKAS 300  
 DB 241 EYGRPTLEVPNVCHSNISYPKETIPEARS DMHYSVAEGLKPAAPARNAFYPCDKAS 300  
 QY 301 KEERPESSDEIALHFEPPNAPLNKGLVSPQSPKSDCCPNSTPTEACSSKNACILQASG 360  
 DB 301 KEERPESSDEIALHFEPPNAPLNKGLVSPQSPKSDCCPNSTPTEACSSKNACILQASG 360  
 QY 361 SPPAKSPTDPKACMCKKXKFIIVNSLQNAKPGPEQAEIGRLSPRAYTAPPAQOPMPEP 420  
 DB 361 SPPAKSPTDPKACMCKKXKFIIVNSLQNAKPGPEQAEIGRLSPRAYTAPPAQOPMPEP 420  
 QY 421 ENLDOSPTKLSASGEDSTIPOASRLNNIYNRSMTGSPRSSSHSPLYNHMPKCTSCGS 480  
 DB 421 ENLDOSPTKLSASGEDSTIPOASRLNNIYNRSMTGSPRSSSHSPLYNHMPKCTSCGS 480  
 QY 481 QSPQHAMCMTHTAGPTAEEMGETQSEYSDSSCENGAFCNECDRCRSEASLKRHTLOT 540  
 DB 481 QSPQHAMCMTHTAGPTAEEMGETQSEYSDSSCENGAFCNECDRCRSEASLKRHTLOT 540  
 QY 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTEKPYPCICGTRFRHLQTLKSHLRHTGEKPYHC 600  
 DB 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTEKPYPCICGTRFRHLQTLKSHLRHTGEKPYHC 600  
 QY 601 PYKCTCGARFVOVAHLRAVHLIHTGEKPYPCICGTRFRHLQTLKSHLRHTGEKPYHC 660  
 DB 601 PYKCTCGARFVOVAHLRAVHLIHTGEKPYPCICGTRFRHLQTLKSHLRHTGEKPYHC 660  
 QY 661 EKNLHFRHKSQRLRLHROKGAITNTKQVRYVSATDLPPELPRAC 706  
 DB 661 EKNLHFRHKSQRLRLHROKGAITNTKQVRYVSATDLPPELPRAC 706

RESULT 5  
 US-09-761-117-2  
 Sequence 2, Application US/09761117  
 Patent No. US20010012887A1  
 GENERAL INFORMATION:  
 APPLICANT: Dalla-Favera, Riccardo  
 APPLICANT: Chaganti, Raju S.K.  
 TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS  
 TITLE OF INVENTION: bcl-6  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10036



Db 135 -----YEPGIS----- 141  
Qy 235 ARPVGYSRPTLEVPNVCHSNISYSPKETTPEBARSDMHYSVAEGLKPAASARNAPYF 294  
Db 142 -----LRPL----- 145  
Qy 295 PCDKASKEERPSSEDEIALHPEPPNAPLNKGLVSPQSDQCPNSPTACSSKNAC 354  
Db 146 -----EABPPT-----PPTAP-----PGSPRRSGHDPPTESRS----- 176  
Qy 355 ILQAGSPPAKSPDPAACNWKYKFTVLSNINAKPGPEOAEGLSPRAYTAPAC 414  
Db 177 ---CSQGPSPASDPDPAACNWKYKFTVLSNINAKPGPEOAEGLSPRAYTAPAC 223  
Qy 415 QPMEPENLDQSPTKLSASGEDSTIP-QASRLNINVRSMTGSPRSSSHSPLVMP 473  
Db 224 QARLPDDEASSSSSSSSSEBGPDPGOSRL-----SPTATVOF----- 265  
Qy 474 KCTSCGSPQHAEMCHTAGPTAEEMGETQSEYSDSCENGAFPCNECCRSSEASL 533  
Db 266 ---KCG--APASTPYLLTSQ---AODTSGSPSRARPLPSBEPFSCNCEAVAGCSSGL 316  
Qy 534 KRHTLQTHSDKPYKCDRCQASFRYKGNLASHKVTHTGKPYKNCICGAQFNRPANLKTHT 593  
Db 317 D-SLVPGDEDEKPYKCDRCQASFRYKGNLASHKVTHTGKPYKNCICGAQFNRPANLKTHT 375  
Qy 594 RIHSGEKYKCECTCGARFVOVAHLRAVLIHTGKPYPCICGTRFRHLQTLKSHLRHT 653  
Db 376 RIHSGEKYKCECTCGARFVOVAHLRAVLIHTGKPYPCICGTRFRHLQTLKSHLRHT 435  
Qy 654 GEKPYHCEKCNLHFRHKSQRLHLRQKHGAITNTKVQYRV 693  
Db 436 GEKPYHCDPCGLHFRHKSQRLHLRQKHGAITNTKVHYHI 475

RESULT 7  
US-10-211-462-24  
; Sequence 24, Application US/10211462  
; Publication No. US20040033495A1  
; GENERAL INFORMATION:  
; APPLICANT: Murray, Richard  
; APPLICANT: Glynn, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of diagnosis of Angiogenesis. Compositions and  
; FILE REFERENCE: 018501-006200US  
; CURRENT FILING DATE: US/10/211,462  
; PRIOR FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US 09/784,356  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/791,390  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: US 60/310,025  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/334,244  
; PRIOR FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 230  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-211-462-24

Query Match 30.5%; Score 1155; DB 4; Length 479;  
Best Local Similarity 38.3%; Pred. No. 2,6e-67;  
Matches 268; Conservative 58; Mismatches 142; Indels 232; Gaps 15;

Qy 1 MASPA--DSCI-----QFTRHASDVLTNLRSLRDLTDVIVVSRQGFRAHKTIVLMACS 54  
Db 1 MASPAFEGALGVYVEFTTHSSSDVIGNLRLRGLITDVTLLVGGQPLRAHKAVALIACS 60

Qy 55 GLEYSITFDQKCNLSYINLDPEINBEGFILLDPWYTSRLNIREGINAMVATAMYLQ 114  
Db 61 GFYSIFRGAGVGVVDLSLPGCBARGFAPLDPMITSLRLSRPATAPVLAATYLO 120  
Qy 115 EHVDTCKRFKIKASEAMVSAIKPREEFLNSRLMPODIWAYGREVENNLPLRSAPG 174  
Db 121 EHVQACHRTIQS----- 134  
Qy 175 CESRAFAPSLSGLSTPPASYSMTSHLPVSLLPSEDEFDVMPPVANPPKRALPCDS 234  
Db 135 -----YEPGIS----- 141  
Qy 235 ARPVGYSRPTLEVPNVCHSNISYSPKETTPEBARSDMHYSVAEGLKPAASARNAPYF 294  
Db 142 -----LRPL----- 145  
Qy 295 PCDKASKEERPSSEDEIALHPEPPNAPLNKGLVSPQSDQCPNSPTACSSKNAC 354  
Db 146 -----EABPPT-----PPTAP-----PGSPRRSGHDPPTESRS----- 176  
Qy 355 ILQAGSPPAKSPDPAACNWKYKFTVLSNINAKPGPEOAEGLSPRAYTAPAC 414  
Db 177 ---CSQGPSPASDPDPAACNWKYKFTVLSNINAKPGPEOAEGLSPRAYTAPAC 223  
Qy 415 QPMEPENLDQSPTKLSASGEDSTIP-QASRLNINVRSMTGSPRSSSHSPLVMP 473  
Db 224 QARLPDDEASSSSSSSSSEBGPDPGOSRL-----SPTATVOF----- 265  
Qy 474 KCTSCGSPQHAEMCHTAGPTAEEMGETQSEYSDSCENGAFPCNECCRSSEASL 533  
Db 266 ---KCG--APASTPYLLTSQ---AODTSGSPSRARPLPSBEPFSCNCEAVAGCSSGL 316  
Qy 534 KRHTLQTHSDKPYKCDRCQASFRYKGNLASHKVTHTGKPYKNCICGAQFNRPANLKTHT 593  
Db 317 D-SLVPGDEDEKPYKCDRCQASFRYKGNLASHKVTHTGKPYKNCICGAQFNRPANLKTHT 375  
Qy 594 RIHSGEKYKCECTCGARFVOVAHLRAVLIHTGKPYPCICGTRFRHLQTLKSHLRHT 653  
Db 376 RIHSGEKYKCECTCGARFVOVAHLRAVLIHTGKPYPCICGTRFRHLQTLKSHLRHT 435  
Qy 654 GEKPYHCEKCNLHFRHKSQRLHLRQKHGAITNTKVQYRV 693  
Db 436 GEKPYHCDPCGLHFRHKSQRLHLRQKHGAITNTKVHYHI 475

RESULT 8  
US-09-815-379-4  
; Sequence 4, Application US/09815379  
; Publication No. US20030073613A1  
; GENERAL INFORMATION:  
; APPLICANT: RASTELI, LUCA  
; APPLICANT: GERITSEN, MARY  
; TITLE OF INVENTION: ANGIOGENESIS ASSOCIATED PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE: 10716/35  
; CURRENT FILING DATE: US/09/815,379  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: 60/191,134  
; PRIOR FILING DATE: 2000-03-22  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-815-379-4

Query Match 29.6%; Score 1122.5; DB 3; Length 518;  
Best Local Similarity 36.3%; Pred. No. 3.8e-65;  
Matches 268; Conservative 58; Mismatches 142; Indels 271; Gaps 17;

Qy 1 MASPA--DSCI-----QFTRHASDVLTNLRSLRDLTDVIVVSRQGFRAHKTIVLMACS 54

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Db      1  MGSPPAPBGAIGVREFTTHSSDVLCNMBELRGILTTVTLLVGQPLRAKAVLIACS 60
Qy      55  GLFYSITFDOLKCNLSVINLDPREINDEGFCILLDFMYTSRLNREGNINAVATAMYLQ 114
Db      61  GFPTYSIFRGAGVGVVLSLPGPBARGAPLLDFMYTSRLSPATAVAALAAATYLOM 120
Qy      115  EHVVDCTCKFIKASEAMVSATPPREEFPLNSMLMPODIMVGRGEVENNLPLRSARG 174
Db      121  EHVVAQCHRTQAS----- 134
Qy      175  CESRAAPSLYSGLSTPPASYSWYSHLPVSSLLFSDREFDVAMPVNPFPKERALPCDS 234
Db      135  -----YEPGLIS----- 141
Qy      235  ARPVEYSRPTLEVSPNVCHSNISPKETIPREARSDMHYSVAGLKCPAAPSARNAPYF 294
Db      142  -----LRPL----- 145
Qy      295  PCDKASKEERPSSEDEIALHFEPPNAPLNRKGLVSPQSPQSDCCPNSTACSSKNAC 354
Db      146  -----EAPPT-----PPTAP-----PGSPRRSEGHDPPTESRS----- 176
Qy      355  ILQASGSPKASPTDPPACMKKCYKFIVLNSLNQNAKPGGPBOAELGRLSPRAYTAPAC 414
Db      177  ---CSGQSPSPADPDKACMKKTKYIVANS-----QASQAGSLVGERSSGQPCP 223
Qy      415  QPPM-BPENLDLOSPTKLSASGEDSTIP-QASRLNINIVRSMTSPRSSSESHPLYMHP 472
Db      224  QALPBGDEASSSSSSSSSESGPIPGQSRL-----SPTAATVCP----- 266
Qy      473  PKCTSCGSSQSPQAEMLHTAGPTFAEMGETOSEVSDSCENGATFCNECDORSEBAS 532
Db      267  ----KCG--APASTPYLLTSQ-----AQDTSGSPSEBARPLPGSEFSCONCEAVACSSG 316
Qy      533  LKXHTLOTSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYKNCIQAQFNRPANILKTH 592
Db      317  LD-SLVPGDEDKPYKQOLCSSFRYKGNLASHKTVHTGKPYKNCIQAQFNRPANILKTH 375
Qy      593  TRIHSGEKPYKCETCGARFY-----QY 614
Db      376  SRHSGEKPYKCETCGARFYQVRSQPSGFGKPARGVGQKGFSSQKQDLKSPSPG 435
Qy      615  AHRRAHVLITGKPYKCEICGTRFRILQTLKSHLRHTGKPYKCEKCNLHRRHSQAR 674
Db      436  AHRRAHVLITGKPYKCEICGTRFRILQTLKSHLRHTGKPYKCEKCNLHRRHSQAR 495
Qy      675  LHLRQKHGALINTKVOYRV 693
Db      496  LHLRQKHGALINTKVMYHI 514

RESULT 9
US-10-974-440-27
; Sequence 27, Application US/10974440
; Publication No. US20050214795A1
; GENERAL INFORMATION:
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: REDDY, Roopa
; APPLICANT: TANG, Y. Tom
; APPLICANT: GERSTIN, Edward H.
; APPLICANT: ARVIZU, Chandra
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LU, Dying Alina M.
; TITLE OF INVENTION: Human Transcriptional Regulator Molecules
; FILE REFERENCE: PE-0509 USN
; CURRENT APPLICATION NUMBER: US/10/974,440
; CURRENT FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: US/09/674,743

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; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/09935
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/084,254
; PRIOR FILING DATE: 1998-05-04
; PRIOR APPLICATION NUMBER: 60/095,827
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/102,745
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PERL Program
; SEQ ID NO 27
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 1484257CD1
US-10-974-440-27

Query Match      16.3%; Score 618.5; DB 5; Length 810;
Best Local Similarity 26.7%; Pred. No. 6,8e-32; Indels 149; Gaps 24;
Matches 200; Conservative 102; Mismatches 199

Qy      9  IOPTRHASPVLNLRNLSRDLITDVIVVSRQOPRAHKTVMACSGLFYSITFDOLKCN 68
Db      1  MDPFQHSQVLSQALNQKQRLGILCTCFYDGVHFKAHAVLAACSERYKMLFVQD---- 56
Qy      69  LSVINLDPREINDEGFCILLDFMYTSRLNREGNINAVATAMYLQMEHVVDCTCKFIKAS 128
Db      57  KQVHLHDS-NAAGLGQVLEFMYTAKLSLSPENVVDVLAVALFLOQODIITACH----- 109
Qy      129  EAMVVSATPPREEFPLNSMLMPODIMVGRGEVENNLPLRSARGCESRA----FAPSL 184
Db      110  -----ALKSLAE-----PATSPGNABALAKQCPVPS-PEGDGRAABEKVATST 153
Qy      185  VS-----GLSTP--PASYSWYSHLPVSSLLFSDREFDVAMPVNPFPKERALPCDSARP 237
Db      154  LSRLEQAGSTPIGSS-----RDJK-----BERGGQAGSAAS 185
Qy      238  VPGEYSRPTLEVSPNVCHSNISPKETIPREARSDMHYSVAGLKCPAAPSARNAPYPCD 297
Db      186  GAEQTEKAD-----APREPPVELKPDPTSGMAALEAALSESSBDEMEVE 232
Qy      298  KASKEERPSSEDEIALHFEPPNAPLNRKG--LVSPQSPQSDCCPNSTACSSKNACI 355
Db      233  PARKSEEQKEQEBQEEGAGP-AEYKEKSQLENGAEENEENESAGTDSGQELG-- 289
Qy      356  LQASG--SPKASPTDPA-----CNMKKYFIVLNSLNQNAKPGGPBOAELGRLSPR 406
Db      290  -EARGLRSGTYGDRITSKAYGVYHKCEDCGKGFHTTGNFHXHIRHTGKPYKCEKCGK 348
Qy      407  AYTAPACQPMPEPENLDQSPTKLSASGEDSTIPQASRLNINIVRSMTSPRSSSESHS 466
Db      349  AFSDPAAACE-----ANEKTHSLPKYGCCEGKSYRLISLNLHKKRHSGEARVRCEDG 403
Qy      467  PLY-----NA-----PKCTSCGSSQSPQAEMLCHTAGPTFAEMGETOSEVSDS 511
Db      404  KLFITTSGNLKHQLVHSGEKPQDCYCGRSFSDPTSKMHL-----FTHDHDKHKCP 456
Qy      512  SCE-----NGAFPCNECDRCFSEESALSKHTTLOTHS-DKPYKCDRCQ 552
Db      457  HCDKKNQVGNLKAHLKIHADPLKCRGCGKQFTTSGNLKHH-LRIHSGEKPYVLCIHQ 515
Qy      553  ASFRYKGNLASHKTVHTGKPYKNCIQAQFNRPANILKTHTRIHSGEKPYKCETCGARFY 612
Db      516  RQPADPGALQHRVHRTGKPYKQCVWCGKAFQASLSLHNVQHTGKPYKCEKCRKRFV 575
Qy      613  QVAHLRAHVLITGKPYKCEICGTRFRILQTLKSHLRHTGKPYKCEKCNLHRRHSQ 672
Db      576  QSSQLNHRIRHNDNIRPHKCSVCSKAFVNVGDSLKHIIHTGKPYLCKDCGGRFVRVDN 635
Qy      673  LRLHLRQKHGALINTKVOYRVSATDLPPE 701

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Db      67 LDVK-IVSGIGQLDPMYTHSLDNDNQVMDTQCIQYQVNVLSLCHTFLEKSA----- 120
Qy      134 SAIKPRREFEFLSRMLMPDIDIMAYRGREVENNLPILRSAPCCSRRAPASGLSTPPA 193
Db      121 TVVQPPG-----MP-----CNSTL---SLQSTL-TPDA 144
Qy      194 SYEMSYHLPVSSLL-PSDEFRDVRMVPANPFKERALPCDSARPVGEGSRRTLVSPN 252
Db      145 TCVISSEYPPHLOEGSADQCKTIDESH-HPSPVNHHSAGISKQAPPTSDG 200
Qy      253 VC-----HSNIVSPKETIPERARSDMHSVAEGLPAPASANNAPYPCDKASKEERP 306
Db      201 SCETELPFKQPNYYKLRNF-----YSKQYHKAAGPS-----QERVENQ 240
Qy      307 ---SSEDEIHLFEPPNAPLNKGLVSPQS-PQSDCCQNSPTEACSSKNACITLQASG 361
Db      241 FAEISTDTLTVESOPAVSHSECTLESPEHLPSNFLAQPVNDSDAPHPESDARCOQ---- 296
Qy      362 PPAKSPTPDKACMVKYKFIVLNSLQNAKPGPBDQELGRLSRAYTAPAPACQPMPE 421
Db      297 -PVQKRLKKAHLKLN------LKSQY----AEQVSEK 328
Qy      422 NLDIQSPTKLASGSDSTIPQASRLNNIVNRSMTGSPRSSSESHSPLVMHPKCTSCGSG 481
Db      329 SDD--GLTKRLBASAKNTLEKAS-----SQ 351
Qy      482 SPQHAEMCHTAGPTAEENGEGTOSYSOSSCENGAFPCNECCDRSEBASLKRHTLQTH 541
Db      352 SAEKE-----SEEV-----VSCEN--FNCSLSETEREDPALMEDQSTQ 390
Qy      542 SDRPYKCDRCQAFRYKGNLASHKVTYTGKPYRCNIGAQFNPANLKHTRHSGEK 601
Db      391 SQQYALDELCKPFPKSNLHRSHTGKPRECNICGHSFQAGNLQTHLRHSGEK 450
Qy      602 YKCEGAFVQVAHLRAVLIHTGEKPYCEICGTRFRHLQTLKSHRLHTGEKPYHC 661
Db      451 YICEIGKRAASGDVQRHIIHSGEKPHICDLCGSGFSNFSMLKHKHTHTADYVFTCD 510
Qy      662 KNLHFRHNSQLRLHQRKGALTTNTKVQYVSATDLPPLPAC 706
Db      511 ECGKSFNMQRKL-----VKRIHRTGERPYSCSAC 540

RESULT 12
US-09-107-058-9
; Sequence 9, Application US/09107058
; Patent No. US20010010922A1
; GENERAL INFORMATION:
; APPLICANT: Dalla-Favera, Riccardo
; TITLE OF INVENTION: CLONING AND USES OF THE GENETIC
; TITLE OF INVENTION: LOCUS bc1-6
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,058
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678

```

```

; REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-107-058-9

Query Match      14.8%; Score 560; DB 3; Length 110;
Best Local Similarity 99.1%; Pred. No. 3,9e-29;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CIOFTRHASDVLLNINLRSDILTDVVIIVSREQFRARHTVLMACSGLFSIFTDQKLC 67
Db      1 CIOFTRHASDVLLNINLRSDILTDVVIIVSREQFRARHTVLMACSGLFSIFTDQKLC 60
Qy      68 NLSVINLDEINPEGFCILLDPYTSRLNLRGNIMAVATMYLQMEHY 117
Db      61 NLSVINLDEINPEGFCILLDPYTSRLNLRGNIMAVATMYLQMEHY 110

RESULT 13
US-09-761-117-9
; Sequence 9, Application US/09761117
; Patent No. US20010012887A1
; GENERAL INFORMATION:
; APPLICANT: Dalla-Favera, Riccardo
; TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
; TITLE OF INVENTION: bc1-6
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/761,117
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-761-117-9

Query Match      14.8%; Score 560; DB 3; Length 110;
Best Local Similarity 99.1%; Pred. No. 3,9e-29;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CIOFTRHSDVLLNLRSLRDLITDVIVVSREOFRAKTVLMACSGLFYSIFTDQKCNLSYN 67  
 DB 1 CIOFTRHSDVLLNLRSLRDLITDVIVVSREOFRAKTVLMACSGLFYSIFTDQKCNLSYN 60

QY 68 NLSVINLDPINPBGFCILLDFWYTSRLNREGNIMAVMATYLOMEHV 117  
 DB 61 NLSVINLDPINPBGFCILLDFWYTSRLNREGNIMAVMATYLOMEHV 110

RESULT 14  
 US-10-164-359-3  
 ; Sequence 3, Application US/10164359  
 ; Publication No. US20030012776A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chin, Khew-Voon  
 ; TITLE OF INVENTION: Nucleic Acid and Protein Expressed Thereby and Their Involvement  
 ; FILE REFERENCE: 601-1-108US  
 ; CURRENT APPLICATION NUMBER: US/10/164,359  
 ; PRIOR FILING DATE: 2002-08-06  
 ; PRIOR APPLICATION NUMBER: PCT/US00/33438  
 ; PRIOR FILING DATE: 2000-12-07  
 ; PRIOR APPLICATION NUMBER: 60/169,418  
 ; PRIOR FILING DATE: 1999-12-07  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 108  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-164-359-3

Query Match 14.6%; Score 552; DB 4; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-28;  
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 HASDVLLNLRSLRDLITDVIVVSREOFRAKTVLMACSGLFYSIFTDQKCNLSYN 73  
 DB 1 HASDVLLNLRSLRDLITDVIVVSREOFRAKTVLMACSGLFYSIFTDQKCNLSYN 60

QY 74 LDPEINPBGFCILLDFWYTSRLNREGNIMAVMATYLOMEHV 121  
 DB 61 LDPEINPBGFCILLDFWYTSRLNREGNIMAVMATYLOMEHV 108

RESULT 15  
 US-10-477-646-21  
 ; Sequence 21, Application US/10477646  
 ; Publication No. US20050176629A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Andrews, William H.  
 ; APPLICANT: Fraser, Stephanie  
 ; APPLICANT: Foster, Christopher A.  
 ; APPLICANT: Briggs, Laura  
 ; APPLICANT: Mohammadpour, Hamid  
 ; TITLE OF INVENTION: TELOMERASE EXPRESSION REPRESSOR PROTEINS  
 ; TITLE OF INVENTION: AND METHODS OF USING THE SAME  
 ; FILE REFERENCE: SIER-014  
 ; CURRENT APPLICATION NUMBER: US/10/477,646  
 ; PRIOR FILING DATE: 2003-11-12  
 ; PRIOR APPLICATION NUMBER: 60/275,691  
 ; PRIOR FILING DATE: 2001-03-13  
 ; PRIOR APPLICATION NUMBER: 60/275,681  
 ; PRIOR FILING DATE: 2001-03-13  
 ; PRIOR APPLICATION NUMBER: 60/275,689  
 ; PRIOR FILING DATE: 2001-03-13  
 ; PRIOR APPLICATION NUMBER: PCT/US02/07918  
 ; PRIOR FILING DATE: 2002-03-12  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 21

LENGTH: 688  
 TYPE: PRT  
 ORGANISM: human  
 US-10-477-646-21

Query Match 14.2%; Score 540; DB 5; Length 688;  
 Best Local Similarity 25.0%; Pred. No. 7.7e-27;  
 Matches 190; Conservative 103; Mismatches 270; Indels 196; Gaps 29;

QY 11 FTRHSDVLLNLRSLRDLITDVIVVSREOFRAKTVLMACSGLFYSIFTDQKCNLSYN 70  
 DB 5 FVQHSVRVLOELNKKOREKQYCDATLDVGLVFKAMSVLACSHFQSLYDGGSGSV- 63

QY 71 VINLDPINPBGFCILLDFWYTSRLNREGNIMAVMATYLOMEHV 126  
 DB 64 VINLDPINPBGFCILLDFWYTSRLNREGNIMAVMATYLOMEHV 114

QY 127 ASEAEVNSAIKPPREFFLNSRLMPDIMA YRGREVENNLPLRSAPGCSRAFPADSLYS 186  
 DB 115 ASEAEVNSAIKPPREFFLNSRLMPDIMA YRGREVENNLPLRSAPGCSRAFPADSLYS 128

QY 187 GLSTPPASYSMTSHLVSSLLFSDERFDVPMVNPFPKERALPCDSAPVPGEYSRPT 246  
 DB 129 GLG-PPASQVNSHVKPEAGLEEEVSRITGL-VPKDE-PPGSHSP-ORPQ 176

QY 247 LEVSPVNCNSNIYSPKETTPEBARSDMYSVAEGLKPA-APSARNAPYPCDKASK 301  
 DB 177 LEVSPVNCNSNIYSPKETTPEBARSDMYSVAEGLKPA-APSARNAPYPCDKASK 222

QY 302 BEERPSSEDEIALHFE-PNAPLNKGLVSPQSPKSDQCPNSPTACSSKN 352  
 DB 223 QLOGGSEMEVVOVEDDGDGYMSRPAVLTR-KSVIVKPKCAAB 269

QY 353 ACTLOASGSPRAPS-PTDPKACNMK-KYFIVLNSLNQNAKPGCPQABELGRL 403  
 DB 270 ALSAGSLAEPAPENRGTAVPECPCHKKFLSKYILKVNRRKHTGSKP- 318

QY 404 SPRAVYTPPACQPMPEPNDLOSPTKLSASGSDSTIPQSRNNIYNRS-MTQSP- 458  
 DB 319 SPRAVYTPPACQPMPEPNDLOSPTKLSASGSDSTIPQSRNNIYNRS-MTQSP- 356

QY 459 RSSSESHSPLYMH-PPCTSGSQSPQHAEMCLHT-AGTPAE-E 500  
 DB 357 ETRRRRMLAVHVSHTGEMPYKSSQCPMOKDQSHMITLHGAPKPHACTCAKCF 416

QY 501 MGETOSEYSDSCENG-AEFCNECDRFSSEASLKHITLQTH-SDKPYKCDRCQASFRY 557  
 DB 417 LSRTLEQLHAPFKHRSKCLFVCECEGHRASSRNGLOHIIKAKHNERPHVCEFSHAFTQ 476

QY 558 KGNLASHKTVHTEGKPYRCNICGAQFNRPANLKHTRIHGEEKPYKCTGCAFPVQVAHL 617  
 DB 477 KANLNMHLRHTHTEGKPYRCNICGAQFNRPANLKHTRIHGEEKPYKCTGCAFPVQVAHL 536

QY 618 RAHVLTHTEGKPYRCNICGAQFNRPANLKHTRIHGEEKPYKCTGCAFPVQVAHL 676  
 DB 537 LRHVASHHQBGRPHFCQICGTFKAVQVQLVHARRHGVKFBCTEGCYFTTROAHLRRH 596

QY 677 LRQHGAIYNTKVQYR-VSATDLPPEL 702  
 DB 597 M-EIHDRVENVNPPQRKLRNLIIEDEKGVVVALQPPAEL 634

Search completed: March 2, 2006, 04:10:17  
 Job time: 169 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 2, 2006, 03:50:01 ; Search time 43 Seconds  
(without alignments)

1579.745 Million cell updates/sec

Title: US-10-755-889-18

Sequence: 1 MASPADSCIOFTRHNSVDLL.....TKYQVRSATDLPPELPKAC 706

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3793	100.0	706	A48752	B-cell CLL/Lymphom
2	3777	99.6	706	I52586	B-cell CLL/Lymphom
3	1151.5	30.4	480	JC7812	BCL6 homologous zi
4	602.5	15.9	794	S59069	Z13 protein - mus
5	552	14.6	688	A56360	zinc finger protei
6	522.5	13.8	610	JC7315	myoneurin - human
7	501	13.2	673	S36336	probable transcrip
8	495	13.1	595	G02075	transcription repr
9	491.5	13.0	676	I50643	gammaBp-C - chick
10	491.5	13.0	701	T14757	hypothetical prote
11	479	12.6	693	I37570	zinc finger protei
12	478.5	12.6	1191	S35305	zinc finger protei
13	476	12.5	555	I53869	zinc finger protei
14	474.5	12.5	728	A48830	probable transcrip
15	468.5	12.4	803	A22831	finger protein 1,
16	468	12.3	428	S26823	zinc finger protei
17	463.5	12.2	710	I48668	zinc finger protei
18	460.5	12.1	686	A4612	zinc finger protei
19	454.5	12.0	469	I38600	zinc finger protei
20	454.5	12.0	427	A35659	knirpel-related p
21	453.5	12.0	553	S22954	finger protein zfp
22	450.5	11.9	209	S47068	finger protein HZF
23	446.5	11.8	519	A28073	transcription acti
24	445.5	11.7	466	1 TWRF	transcription fact
25	443	11.7	594	I12488	hypothetical prote
26	442.5	11.7	347	S00549	developmental cont
27	442.5	11.7	580	A37107	spermatogenesis pr
28	442	11.7	292	S43826	finger protein OZF
29	441	11.6	169	A39240	finger protein mtg

30	440.5	11.6	474	2	I54338	zinc finger protei
31	440	11.6	393	2	JN0533	finger protein pML
32	439.5	11.6	411	2	S10245	finger protein, te
33	438.5	11.6	651	2	B32891	finger protein 2,
34	437	11.5	201	2	I57505	zinc finger protei
35	436	11.5	576	2	A48157	renal transcrip
36	435	11.5	543	2	B34612	zinc finger protei
37	433.5	11.4	542	2	A54661	zinc finger protei
38	433.5	11.4	614	2	JH0500	zinc finger protei
39	432.5	11.4	475	2	S03679	finger protein (cl
40	432	11.4	386	2	T12527	hypothetical prote
41	429.5	11.3	455	2	T42670	hypothetical prote
42	428	11.3	247	2	S47070	finger protein HZF
43	426.5	11.2	1350	2	S00647	finger protein - A
44	424.5	11.2	325	2	I38616	zinc finger protei
45	423.5	11.2	675	2	S51037	zinc finger protei

#### ALIGNMENTS

##### RESULT 1

A48752  
B-cell CLL/Lymphoma 6 (BCL6) protein - human  
N/Alternate names: zinc finger transcription factor BCL-6  
C/Species: Homo sapiens (man)  
C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 01-Dec-2000  
C/Accession: A48752  
R/ye, B.H.; lista, F.; Coco, F.L.; Knowles, D.M.; Offit, K.; Chaganti, R.S.K.; Dalla-Fa  
Science 262, 747-750, 1993  
A/Title: Alterations of a zinc finger-encoding gene, BCL-6, in diffuse large-cell lymph

A/Reference number: A48752; PMID:94053709; PMID:8235596

A/Accession: A48752

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-706 <YEA>

A/Cross-references: UNIPARC:UPI000016B151; GB:U00115; NID:G392426; PIDN:AAC50054.1; PID

A/Genetic: A/Gene: GDB:BCL6; BCL5; LA23; ZNF51

A/Cross-references: GDB:138176; OMIM:109565

A/Map position: 3q27-3q27

C/Superfamily: B-cell CLL/Lymphoma 5 protein; POZ domain homology

C/Keywords: transcription factor; zinc finger

F/18-121/Domain: POZ domain homology <POZ>

F/520-541/Region: zinc finger CCHH motif

F/548-568/Region: zinc finger CCHH motif

F/576-596/Region: zinc finger CCHH motif

F/604-624/Region: zinc finger CCHH motif

F/632-652/Region: zinc finger CCHH motif

F/660-681/Region: zinc finger CCHH motif

Query Match 100.0%; Score 3793; DB 2; Length 706;

Best local similarity 100.0%; Pred. No. 3.6e-218;

Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MASPADSCIOFTRHNSVDLLNLRKRDILTDVVIYVSSQEPRAHTVLMACGLFYSI	60
DB	1	MASPADSCIOFTRHNSVDLLNLRKRDILTDVVIYVSSQEPRAHTVLMACGLFYSI	60
QY	61	FTDOLKCNLSVINLNDPEINPEGFCILDPMTSLNLRKRDILTDVVIYVSSQEPRAHTVLMACGLFYSI	120
DB	61	FTDOLKCNLSVINLNDPEINPEGFCILDPMTSLNLRKRDILTDVVIYVSSQEPRAHTVLMACGLFYSI	120
QY	121	CRKRTIKASEAMVSAIKPRPEFLNSRLMPDIMAAYRGREVENNLPLRSAPGCSRAAF	180
DB	121	CRKRTIKASEAMVSAIKPRPEFLNSRLMPDIMAAYRGREVENNLPLRSAPGCSRAAF	180
QY	181	APSLYSGLSTPPASYSWYSLPVSGLPSEERPDVMPVAPNPPKRAIPCDGARVPVG	240
DB	181	APSLYSGLSTPPASYSWYSLPVSGLPSEERPDVMPVAPNPPKRAIPCDGARVPVG	240
QY	241	EYSRPTLEVPNVVHNSNIYSPKERTIPREARDMYSVAEGLKPAAPARNAFYPCDKAS	300
DB	241	EYSRPTLEVPNVVHNSNIYSPKERTIPREARDMYSVAEGLKPAAPARNAFYPCDKAS	300

Db 241 EYSRPTLEVS PNVCHSNIVSPKRTIPEBARSDMHSVABGLKPAAPSAARNAPYPCDDKAS 300  
 QY 301 KEERSSSDEIATLHPEPPNAPLNKGLVSPQSPQSDCOQNSPTPACSSKNACTIQASG 360  
 Db 301 KEERSSSDEIATLHPEPPNAPLNKGLVSPQSPQSDCOQNSPTPACSSKNACTIQASG 360  
 QY 361 SPPAKSPDPAKCNMKKFFIVLNSLNQNAKPGEGQAEIGRLSPRAYTAPACOPMPMP 420  
 Db 361 SPPAKSPDPAKCNMKKFFIVLNSLNQNAKPGEGQAEIGRLSPRAYTAPACOPMPMP 420  
 QY 421 ENLIDQSPTKLSASGEDSTIPQASRLNINVNSMTGSPRSSSSSHSPLYMHPKCTSCGS 480  
 Db 421 ENLIDQSPTKLSASGEDSTIPQASRLNINVNSMTGSPRSSSSSHSPLYMHPKCTSCGS 480  
 QY 481 OSPOHAEMLHTAGPTFPEBEMGETOSEYSDSCENGAFFCNECDGFSSEASLKHRTTLOT 540  
 Db 481 OSPOHAEMLHTAGPTFPEBEMGETOSEYSDSCENGAFFCNECDGFSSEASLKHRTTLOT 540  
 QY 541 HSDKPYKCDRCQASFFYKGNLASHKTVHTGEKPYPCNICGAQPNRPANLKTTRIHSGEK 600  
 Db 541 HSDKPYKCDRCQASFFYKGNLASHKTVHTGEKPYPCNICGAQPNRPANLKTTRIHSGEK 600  
 QY 601 PYKCTCGARFQVAHLRAHVLHTGEKPYPCNICGTRFRHLQTLKSHLRHTGEKPYHC 660  
 Db 601 PYKCTCGARFQVAHLRAHVLHTGEKPYPCNICGTRFRHLQTLKSHLRHTGEKPYHC 660  
 QY 661 EKCNLHFRHKSQRLRLRQKHGAIITNTKQYRVSATDLPPELPKAC 706  
 Db 661 EKCNLHFRHKSQRLRLRQKHGAIITNTKQYRVSATDLPPELPKAC 706  
 RESULT 2  
 152586  
 B-cell CLL/Lymphoma 5 (BCL5) protein - human  
 N:Alternate names: finger protein LAZ-3; zinc finger transcription factor BCL-5  
 C:Species: Homo sapiens (man)  
 C>Date: 01-Nov-1996 #sequence revision 01-Nov-1996 #text\_change 09-Jul-2004  
 R:Accession: 152586; S40520; S32767  
 R:RefSeq: T.; Kawamata, N.; Hirose, S.; Aoki, N.  
 Blood 83, 26-32, 1994  
 A>Title: Gene involved in the 3q27 translocation associated with B-cell lymphoma, BCL5.  
 A:Reference number: 152586; PMID:94100541; PMID:8274740  
 A:Accession: 152586  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-706 <NR>  
 A:Cross-references: UNIPROT:P41182; UNIPARC:UPI000012682C; GB:567779; NID:9459372; PIDN:  
 R:Kerker, J.P.; Dewelndt, C.; Tilly, H.; Quilef, S.; Lecocq, G.; Baastard, C.  
 Nature Genet. 5, 66-70, 1993  
 A>Title: LAZ3, a novel zinc-finger encoding gene, is disrupted by recurring chromosome 3  
 A:Reference number: S40520; MUID:94035122; PMID:8220427  
 A:Accession: S40520  
 A:Molecule type: mRNA  
 A:Residues: 1-706 <NR>  
 A:Cross-references: UNIPARC:UPI000012682C; EMBL:Z21943; NID:9297025; PIDN:CAA79937.1; PI  
 C:Genetics:  
 A:Gene: GDB:BCL5, LAZ-3, ZNF51  
 A:Cross-references: GDB:125178; OMIM:151441; GDB:138176; OMIM:109565  
 A:Map position: 17q22.1;q22.3;q27.3;q27  
 A:Introns: 60/3  
 C:Superfamily: BRCORE-2 protein; POZ domain homology  
 C:Keywords: DNA binding; transcription factor; zinc finger  
 F:18-121/Domain: POZ domain homology <POZ>  
 F:520-541/Region: zinc finger CCH motif  
 F:548-568/Region: zinc finger CCH motif  
 F:576-596/Region: zinc finger CCH motif  
 F:604-624/Region: zinc finger CCH motif  
 F:632-652/Region: zinc finger CCH motif  
 F:660-681/Region: zinc finger CCH motif  
 Query Match 99.6%; Score 3777; DB 2; Length 706;  
 Best Local Similarity 99.6%; Pred. No. 3.2e-217;  
 Matches 703; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTRHSDVLTNLNRLSRDIIITDVYIVVSRBOFRAKTVLMASGLFYYSI 60  
 Db 1 MASPADSCIOFTRHSDVLTNLNRLSRDIIITDVYIVVSRBOFRAKTVLMASGLFYYSI 60  
 QY 61 FTDLKCNLSVINLDEINPBGFCILLDMYTSRLNLRBNIMAVMATMYLQMEHVYDT 120  
 Db 61 FTDLKCNLSVINLDEINPBGFCILLDMYTSRLNLRBNIMAVMATMYLQMEHVYDT 120  
 QY 121 CRKFTKASBAEWSAIAKPPREFLNSRLMPODIAIYAGREVENNLPURSAFGESDAF 180  
 Db 121 CRKFTKASBAEWSAIAKPPREFLNSRLMPODIAIYAGREVENNLPURSAFGESDAF 180  
 QY 181 APSLVSGLSTPPASYSMTSHLPVSSLLPSDEEFVRVNPVAPFPKRALPCDSARPYVG 240  
 Db 181 APSLVSGLSTPPASYSMTSHLPVSSLLPSDEEFVRVNPVAPFPKRALPCDSARPYVG 240  
 QY 241 EYSRPTLEVS PNVCHSNIVSPKRTIPEBARSDMHSVABGLKPAAPSAARNAPYPCDDKAS 300  
 Db 241 EYSRPTLEVS PNVCHSNIVSPKRTIPEBARSDMHSVABGLKPAAPSAARNAPYPCDDKAS 300  
 QY 301 KEERSSSDEIATLHPEPPNAPLNKGLVSPQSPQSDCOQNSPTPACSSKNACTIQASG 360  
 Db 301 KEERSSSDEIATLHPEPPNAPLNKGLVSPQSPQSDCOQNSPTPACSSKNACTIQASG 360  
 QY 361 SPPAKSPDPAKCNMKKFFIVLNSLNQNAKPGEGQAEIGRLSPRAYTAPACOPMPMP 420  
 Db 361 SPPAKSPDPAKCNMKKFFIVLNSLNQNAKPGEGQAEIGRLSPRAYTAPACOPMPMP 420  
 QY 421 ENLIDQSPTKLSASGEDSTIPQASRLNINVNSMTGSPRSSSSSHSPLYMHPKCTSCGS 480  
 Db 421 ENLIDQSPTKLSASGEDSTIPQASRLNINVNSMTGSPRSSSSSHSPLYMHPKCTSCGS 480  
 QY 481 OSPOHAEMLHTAGPTFPEBEMGETOSEYSDSCENGAFFCNECDGFSSEASLKHRTTLOT 540  
 Db 481 OSPOHAEMLHTAGPTFPEBEMGETOSEYSDSCENGAFFCNECDGFSSEASLKHRTTLOT 540  
 QY 541 HSDKPYKCDRCQASFFYKGNLASHKTVHTGEKPYPCNICGAQPNRPANLKTTRIHSGEK 600  
 Db 541 HSDKPYKCDRCQASFFYKGNLASHKTVHTGEKPYPCNICGAQPNRPANLKTTRIHSGEK 600  
 QY 601 PYKCTCGARFQVAHLRAHVLHTGEKPYPCNICGTRFRHLQTLKSHLRHTGEKPYHC 660  
 Db 601 PYKCTCGARFQVAHLRAHVLHTGEKPYPCNICGTRFRHLQTLKSHLRHTGEKPYHC 660  
 QY 661 EKCNLHFRHKSQRLRLRQKHGAIITNTKQYRVSATDLPPELPKAC 706  
 Db 661 EKCNLHFRHKSQRLRLRQKHGAIITNTKQYRVSATDLPPELPKAC 706  
 RESULT 3  
 UC7812  
 BCL6 homologous zinc finger protein BAZF - human  
 C:Species: Homo sapiens (man)  
 C>Date: 03-Jun-2002 #sequence revision 03-Jun-2002 #text\_change 09-Jul-2004  
 R:Accession: UC7812  
 R:Sakshita, C.; Fukuda, T.; Okabe, S.; Kobayashi, H.; Hirose, S.; Tokuhisa, T.; Miyae,  
 Biochem. Biophys. Res. Commun. 291, 567-573, 2002  
 A>Title: Cloning and characterization of the human BAZF gene, a homologue of the BCL6 or  
 A:Reference number: UC7812; PMID:11855826; MUID:21845446  
 A:Accession: UC7812  
 A:Molecule type: DNA  
 A:Residues: 1-480 <NR>  
 A:Cross-references: UNIPROT:Q6N143; UNIPARC:UPI0000072773; DBJ:AB076580; DBJ:AB076581  
 C:Comment: This protein, a zinc finger protein containing a conserved amino terminal BTR  
 rly in the induction of megakaryocytic differentiation to produce mature platelets. This  
 cell fate.  
 C:Genetics:  
 A:Gene: BAZF  
 A:Map position: 17p13.1  
 A:Introns: 60/2; 134/2; 256/2; 297/3; 353/1; 396/3; 442/3  
 C:Keywords: differentiation

[illegible]



A:Title: Fusion between a novel Kruppel-like zinc finger gene and the retinoic acid re  
A:Reference number: S36336; MID:93209216; PMID:8384553  
A:Accession: S36336  
A:Molecule type: mRNA  
A:Residues: 1-673 <GB>  
A:Cross-references: UNIPROT:Q05516; UNIPARC:UPI000013C2FE; EMBL:Z19002; NID:G38517; PIDN  
C:Genetics:  
A:Gene: PUF  
C:Keywords: zinc finger  
F:20-118/Domain: POZ domain homology <POZ>

Query Match 13.2%; Score 501; DB 2; Length 673;  
Best Local Similarity 25.9%; Pred. No. 2e-22;  
Matches 186; Conservative 102; Mismatches 286; Indels 144; Gaps 27;

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9 IQFPHASDVLLMLNRSRDLITDVIVVSRQFRAHKTVMACGLFYISITDQKCN 68
11 LQNPSPHTGLCKANQRLAGTICDVIWDSQEFHARTVLACTSKMFIIF--HRN 66
69 LSVINIDPEINPGFCLIDPMYTSRLNREGNIMAVMTAMYLQMEHVVDTCRKFKA- 127
67 SQHYTLD-FLSPKTFQOILEYATATLQAKAEIDIDLVAARILEIETLEEOCLKMETI 125
128 -----SEKPMYSATPPREELNSMLMPQDIAMARGEVENMLPLRSAPG-CESRA 179
126 QASDDNDTEATMDG-GAESEEDRKARYLNKIFSKSSSESGYASVAGSLPEPMVDQS 184
180 FAPSLVSGSLT-PPASYSMTSHLPVSSILFSDEEFDVMPVNPFPKRALPCDSARPV 238
185 PSVSTSGLSAMSTKAAVDSLMITQSL-----LQSTLPPAG--FEPTLACGGRHPG 237
239 PGEYSRPLEVSPVNCSTNYSPKETTPEARSDMHVSVAELKPAAPSAANADPYPCDK 298
238 VAEVKTMMQVDE-----VFSQDSPGALES-----SIGGM----- 268
299 ASKEEPPSEDEIALFEPNMAINKGLVSP-----SPQKSCQCPNSPTACSSKNAC 354
269 GDKVEERGK-----EGGPTTRSSVITSAELHYGRESAEVPPPEAA----- 312
355 ILQASGSPKASPTDPKACMKKCYFIYNSLNONAKRGPGEQALGRLSPRAYTAPAC 414
313 -----GQAPGGRPHAP--PPEKHLCIYSVLNPK-----ADAVLSMPSSTSGLHV 358
415 QPMPENLIDQSPKLSASGEDST--IPQ-----SRLNNVNRMTGSPRSSE 463
359 QP-----ALAVSMDFSTYGLLPQGIQRELFSKLDELAA-VGKKSSRTIGE 404
464 SHSPLVMPKCTSCGSP-----QHAEMCLHTAGFTPAEKGETOSEYSDS----- 511
405 -----QCSVCGVELPONEAVEQHRK--LHSGMKTVCCEL--CGKRLDLSRLMH 450
512 -----SCNGAFPCNECDRSESEASIKRHTLOT--SDPKYKCDRCQASFPYKGNLSHK 565
451 LLAHSAGAKAVCCQCGAQSKEDELETHR-QTHGTDMAVFCLLCGRFQAQSLQOHM 509
566 TVHTGEKPYRCNIGCAQFRRPANIUKTHRIHSGEKPYRCETCGARFVQVAVLRAVLIHT 625
510 EVHAGVRSYISSECKRTPPSHTALKRHSHTGHDPYRCESGCFRFBESTLKSHT 569
626 GEKPYPCICGTRPHHQLTKSHLRITGKPYHCEKNLHFRHKSQRLHLRQKHGA 683
570 GEKPYECGCDKFKSLKHQLETHYVHTGKPECKLCHORSRDYSAMIKHLRTNNGA 627
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RESULT 8  
G02075  
transcription repressor zinc finger protein 85 - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004  
C:Accession: G02075  
R:Portelet, D.A.  
Submitted to the EMBL Data Library, September 1995  
A:Reference number: G09169

A:Accession: G02075  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-595 <PON>  
A:Cross-references: UNIPROT:Q03923; UNIPARC:UPI000013C428; EMBL:U53376; NID:G1017721; P  
C:Genetics:  
A:Gene: GDB:ZNF85  
A:Cross-references: GDB:132279  
A:Map position: 19p12-19p12  
C:Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 13.1%; Score 495; DB 2; Length 595;  
Best Local Similarity 30.8%; Pred. No. 3.9e-22;  
Matches 130; Conservative 54; Mismatches 158; Indels 80; Gaps 16;

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320 NADLNKGLVSPQSPQKSCQPNSPTEACSSKNACTLOASGSPKASPTDPKACMKKYK 379
111 NLPL-RKGCES-----MDCKMKR--GGCNGLMQCL-----TATQSKIFQCDKYV 152
380 FYLNSLNONAKRGPGEQALGRLSPRAYTAPACQPPMEPENLIDQSPKLSAS-GEES 438
153 KVAKFSNSN-----RHEIRTKKK--PKC-----TKCKSPGEMIS 187
439 TIPQASRLNNIVN-----RSMTSPRSSSESHSPLVY--HPKCTSCGSPQHAEM 488
188 CLTEHRIRHRYVAFYKCECGKAFNMS--STLTKHRIHNGEKPYKCECGKAFNQSNTL 245
489 C-----LHTA-GPTFAEMGETOSEYSDSCE-----NGAFNCECDRSEBASLKRHT 537
246 IKKKIHTGKPKYKCECGKAFNRFSTLTKKIHTGKPYKCECGKAFNQSNTLTKHR 305
538 LQTHSDKPYKCDRCQASFRKGNLASHKTYHTEKPYRCNIGCAQFRRPANIUKTHRIHS 597
306 KHTGKPYKCECGKAFNQSNTLTKKIHTGKPYKCKCKGKAFNQSNTLTKHRIHS 365
598 GEKPYKCECGARFVQVAVLRAVLIHTGKPYPCICGTRPHHQLTKSHLRITGKEP 657
366 GEKPYKCECGKAFNHSHTLTKKIHTGKPYKCECGKAFNQSNTLTKHRIHS 425
658 YHCEKNLHFRHKSQRLHLR-----QHGAIYNTK--VQYRVASATDLPBLPK 704
426 YKSECEKAVNQSNTLTKHRIHTGKPYKCECGKAFNQSNTLTKHRIHTEKPYKCE 485
705 AC 706
486 EC 487
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RESULT 9  
150643  
gammaFBP-C - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: 150643; 150641; 150642; 544242; 544264; 544265  
R:Li, O.; Shalaby, F.; Puri, M.C.; Tang, S.; Breitman, M.L.  
Dev. Biol. 165, 165-177, 1994  
A:Title: Novel zinc finger proteins that interact with the mouse gamma F-cytoskeleton  
A:Reference number: 150641; MID:94374565; PMID:8088434  
A:Accession: 150643  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-676 <LNU>  
A:Cross-references: UNIPROT:Q09850; UNIPARC:UPI000012C71A; EMBL:X79011; NID:G475903; PI  
A:Accession: 150641  
A:Molecule type: mRNA  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Residues: 1-676 <LNU>  
A:Cross-references: UNIPARC:UPI000002AB16; EMBL:X79051; NID:G479055; PIDN:CA55653.1; P  
A:Molecule type: mRNA  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Residues: 36-676 <L13>  
A:Cross-references: UNIPARC:UPI000002AB17; EMBL:X79050; NID:G479057; PIDN:CA55652.1; P

C/Superfamily: BRcore-2 protein; POZ domain homology  
F:49-152/Domain: POZ domain homology <POZ>

Query Match 13.0%; Score 491.5; DB 2; Length 676;  
Best Local Similarity 26.0%; Pred. No. 7.4e-22;  
Matches 175; Conservative 81; Mismatches 245; Indels 173; Gaps 29;

```
QY 14 HASDVLTINLRSLRILTDVIVVIREOPRAHKTVMACSGLFYSIFTDQKCNLSVYN 73
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 45 HSRQLQLQNTQRTKFLCDVILVQNALFRAHKILAAASAYLKLIVVND-----NLIN 99
QY 74 LDPE-INPBGFCILDFMTYSRLNT-----REGNIMAVMATYLMQEHVVDTCRKFYKAS 128
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 100 LDHEWYSPGIFRLILDFITGRIGECBPGEQSIGAVLAASYLQIPGVALCKKXK-- 157
QY 129 EAMVSAIRPPREFLNSRLMLQDIMAIRGREVVENNLPKSAPEGSEK-AFAP-SLYS 186
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 158 -----RSGKYCHLRGGVAPYKLR 176
QY 187 GL-STPPASYSMSHLPVSSILFSDSEPRDVRMPVANPPKBRALPCDSARVPVGEYSRP 245
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 177 GLRATTPVIQACTSGTP-----RPVDLQ-----PVEPAADLNTQ--CGELVYS 217
QY 246 TLEVSFNVCHSNITSPEKTIPEEARSDMYSVAEG-----KPAAPSAANAIFYPCDKKAS 300
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 218 ASQGT--LHPHGLCPPE-----RHCSPPCGILDLSKSPGTSQAQ--LIPTRDLL 263
QY 301 KEBERPSEDEIALHFEPP--NAPLNRKGLVSPFSQKSDCOONS-----PTACSSK 351
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 264 PAEPREPS-----LPRHDSPPVSGILAGHPAAYDSPGSGPHGHPATDPRF-- 314
QY 352 NACILQASSPPKASPTDPAK-----CMWKYKFFVLSNLGNAPKRG--EQALEGL 403
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 315 -----TPPAEPPLPRGDRELMTRMKH-----PPLGYLDEGEAEK 353
QY 404 SPRAYTA--PPACOPMER--ENILDIQSPTKLASAGEDSTIIPQ--ASRLNNIVRSMTCSP 458
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 354 LEEEEKABSPRAPQRRYPSVESNDLEPNSISEEGSSBGPSPGALRYCNH--LGYP 412
QY 459 RSSSESHSLYMHPRYCTSCGSGSPQHAEMCLHTAGPTAEEMGETQSEYSDSCENGA 518
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 413 ESTGDN---LYV---CIPCGKGFPSSEQLNAHV-----EAMNEEELYHKAALGAQVP 458
QY 519 FQNECCORPSESESLKRLHTLQTHSDKPRYCDRCQASFRYKGNLASHKTYHTEGKPRCM 578
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 459 FLDKGAGAGDII-----RPRCSCDSKYKDPATLRQHEKTHMLTRPPCTI 506
QY 579 CGAQNRPANLKTHTRIHSGEKPYKCECTGARFVQVAHLRAHVLHTGEKPYCEICGTR 638
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 507 CGKFTQRGMTMTHMNSHLKRFACDACGMRTROYRLTEHMRTHSGEKPYECQVCGAK 566
QY 639 FRHLQTLKSHLRTH 652
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 567 FAQQRNLISHMKH 580
```

RESULT 10  
T14757

hypothetical protein DKFZp572C163.1 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C/Accession: T14757

R/Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, August 1999

A/Accession: T14757

A/status: preliminary

A/molecule type: mRNA

A/residues: 1-701 <MAN>

A/cross-references: UNIPROT:Q9UG02; UNIPARC:UP100006DDA3; EMBL:AL110217

A/experimental source: adult subthalamic nucleus; clone DKFZp572C163

C/genetics:

A/Note: DKFZp572C163.1

C/Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 13.0%; Score 491.5; DB 2; Length 701;  
Best Local Similarity 40.6%; Pred. No. 7.7e-22;  
Matches 91; Conservative 30; Mismatches 86; Indels 17; Gaps 3;

```
QY 472 PPKTSCGSGSPQHAEMCLHT-----AGPTAEEMGETQSEYSDSCENG-----A 517
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 467 PVECNQCGKTFQQRHLCAHQRIHTEKPYECNECGKT---PADNSALRAHRIHTEKPY 523
QY 518 FFCNECDKRFSEASLKHHTLQTHSDKPYKCDRCQASFRYKGNLASHKTHTGKPYRCN 577
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 524 YECNDGKTFPSKTHSLRAHLTRSGEKPYECSECGKTFSEKSYVAHQRVHTGKPYECN 583
QY 578 ICGAQNRPANLKTHTRIHSGEKPYKCECTGARFVQVAHLRAHVLHTGKPYCEICGT 637
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 584 YCGKFPANSTLRVHQRIHTEKSYECNDGKTFQCKHLSHQRIHTEKPYECNECGK 643
QY 638 FRHLQTLKSHLRHTGKPYKCECNLHFRKSLQRLHLROKH 681
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 644 AFAQNSTLRVHQRIHTEKPYECDECGKTFAKALRLVHHTRMH 687
```

RESULT 11  
I37570

zinc finger protein - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004

C/Accession: I37570

R/Abirink, M.; Aveskog, M.; Hellman, L.

DNA Cell Biol. 14, 125-136, 1995

A/Title: Isolation of cDNA clones for 42 different Kruppel-related zinc finger proteins

A/Reference number: I37566; PMID:95169271; PMID:7865130

A/Accession: I37570

A/status: preliminary; translated from GB/EMBL/DBJ

A/molecule type: mRNA

A/residues: 1-693 <RES>

A/cross-references: UNIPROT:Q14588; UNIPARC:UP1000016AACB; EMBL:X78927; NID:9498726; PTC

C/Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 12.6%; Score 479; DB 2; Length 693;  
Best Local Similarity 28.5%; Pred. No. 4.2e-21;  
Matches 141; Conservative 61; Mismatches 188; Indels 104; Gaps 17;

```
QY 195 YSMYSHLPVSSILFSDSEPRDVRMPVANPPKBRALPCDSARVPVGEYSRPLEVSPNV 254
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 208 FQSSHLLQTHQVHT-----VVKPF-----KCVCEGK-----GFSRSTLV----- 244
QY 255 HSNITSPKE--TIPEANSDMHYS-----VAGLKPAAPSAANAIFYPCDKASKKEER 305
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 245 HCKLHSGEKPYNCECGRAFIASHLOEHORIHTEKPY-----FKDTCGKNFR 294
QY 306 PSEDEIALHFEPPANLNRKGLV--SPQSPQSDCOQSPNPTACSSKNACTLQA--SGSP 362
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 295 RSA-----LNHCHVHTGKPYK--CEDCGKCTGSS--NLRHQVHTGK 337
QY 363 PAKSPDPKACNMWKKYKFFVLSNLQNAKPGGPEQALGRLSPRAYTAPACOPMEREPN 422
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 338 PKCEBGCK--CTIQSQPQAHRIHTEKPYKCYGKGFYSSGFQAHQVHTG----- 391
QY 422 LDQSPPTKISAGEDSTIPQASRLNNIVNRSMTCSPRSSSESHSLYMHPRYCTSCGSG 482
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 392 ---EKPYKNEBGKGFMRKIHQVHLVH---TGE-----KPYKCEVCGKAF 432
QY 483 PQHAEMCLHTAGPTAEEMGETQSEYSDSCENGAFFCNECDKRFSEASLKRHTLQTHS 542
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 433 RGSSTYLKHLKHAHSVQK-----DPKCEBGCGQGFNQSSRLDHLQHLHTG 475
QY 543 DKPYKCDRCQASFRYKGNLASHKTHTGKPYRCNICGAQFNRPANLKTHTRIHSGEKPY 602
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 476 EKPYPKCEBGKGFNRADLKHCRHTHTEKPYNCEBGKGVFQASHLLTHQVHSGEKPF 535
```







GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 2, 2006, 03:45:47 ; Search time 187 Seconds  
(without alignments)  
1658.831 Million cell updates/sec

Title: US-10-755-889-18

Sequence: 1 MASPDSCICQTRHMSDVL.....TKQVRVSATDLPPELPKAC 706

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_21.\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3793	100.0	706	3 AAY78793	Aay78793 Human BCL
2	3793	100.0	706	4 AAB29640	Aab29640 Human bcl
3	3793	100.0	706	8 ADL82847	ADL82847 Human PRO
4	3793	100.0	706	8 ADRI4017	ADRI4017 Human NF-
5	3793	100.0	706	9 ADY19590	ADY19590 PRO polyP
6	3777	99.6	706	8 ADRI4065	ADRI4065 Human NF-
7	3777	99.6	706	9 ADY15006	ADY15006 PRO polyP
8	3771	99.4	706	7 ADJ70182	ADJ70182 Human hea
9	3763	99.2	706	2 AAR68743	AAR68743 BCL-6 zin
10	3763	99.2	706	3 AAY78792	Aay78792 Human BCL
11	3602.5	95.0	707	5 ABB57289	ABB57289 Mouse isc
12	1158.5	30.5	458	6 ABM84710	ABM84710 Human dia
13	1155	30.5	479	6 ABU03467	ABU03467 Angiogene
14	1155	30.5	479	7 ABU64323	ABU64323 AAC2-2 pr
15	1155	30.5	479	7 ADN38698	ADN38698 Cancer/an
16	1155	30.5	479	8 ADU99231	ADU99231 AAC2-2 tu
17	1151.5	30.4	480	6 AAO16438	AAO16438 Human nuc
18	1135.5	29.9	480	7 ABU64322	ABU64322 AAC2-1 pr
19	1135.5	29.9	480	8 ADU99228	ADU99228 AAC2-1 tu
20	1122.5	29.6	518	4 AAE11887	AAE11887 Angiogene
21	912.5	24.1	362	9 AEA20968	AEA20968 Novel hum
22	678.5	17.9	667	8 ADP22538	ADP22538 Sea-squir
23	658	17.3	129	9 AEB10947	Aeb10947 Human BCL
24	658	17.3	129	9 AEB10971	Aeb10971 Human BTB

25	618.5	16.3	810	3 AAY73351	Aay73351 HTRM clon
26	610	16.1	803	7 ADD45510	Add45510 Human pro
27	610	16.1	803	8 ADG30638	Adg30638 Human tub
28	609	16.1	803	4 AAM39272	Aam39272 Human pol
29	609	16.1	804	4 AAM41058	Aam41058 Human pol
30	602	15.9	127	9 AEB10948	Aeb10948 Human BCL
31	602	15.9	803	2 AAW81756	Aaw81756 Myc-B1nd1
32	588	15.5	756	7 ADF17459	Adf17459 Mouse IL-
33	564.5	14.9	765	6 ABP96229	ABP96229 Human nuc
34	560	14.8	765	6 ADR09346	ADR09346 Human pro
35	540	14.2	688	5 ABB82513	ABB82513 Human rep
36	535	14.2	775	7 ADC31774	Adc31774 Human nov
37	522.5	13.8	603	4 AAM41821	Aam41821 Human pol
38	522.5	13.8	610	4 AAB53761	Aab53761 Human pro
39	522.5	13.8	610	4 AAB50159	Abb50159 Human tra
40	522.5	13.8	610	5 AAM47779	Aam47779 Human myo
41	522.5	13.8	610	5 AAM47790	Aam47790 Murine my
42	522	13.8	610	5 AAM47925	Adm47925 Human pha
43	518	13.7	706	9 ADY71947	Ady71947 Mouse GZF
44	517	13.6	711	5 AAO21779	Aao21779 Lung-spec
45	517	13.6	711	9 ADY71945	Ady71945 Human GZF

## ALIGNMENTS

RESULT 1  
ID AAY78793 standard; protein; 706 AA.  
XX AAY78793;

AC AAY78793;

DT 19-MAY-2000 (first entry)

XX Human BCL-6 protein sequence.

DE BCL-6; human; B-cell lymphoma; regulator; non-Hodgkin's lymphoma;

KW diffuse type B-cell lymphoma.

OS Homo sapiens.

PN WO20000185-A1.

PD 06-JAN-2000.

XX 30-JUN-1999; 99WO-US014703.

PF 30-JUN-1998; 98US-00107058.

XX 30-JUN-1998; 98US-00107058.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Dalla-Favera R, Niu H;

XX WPL; 2000-160631/14.

XX Novel methods for regulating BCL-6 levels in cells used to treat humans with lymphoma.

XX Example 2; Fig 10; 159pp; English.

This sequence represents the human bcl-6 protein sequence. The invention relates to a vertebrate bcl-6 locus which is the breakpoint cluster region in B-cell lymphomas, and contains a bcl-6 gene encoding a BCL-6 polypeptide. Administration of a molecule which induces phosphorylation of BCL-6 and thereby induces BCL-6 degradation, can be used as a method of regulating BCL-6 in cells. The methods of the invention can be used to regulate, and especially to decrease BCL-6 levels in cells. The methods may also be used to screen putative therapeutic agents for treatment of non-Hodgkin's lymphoma, by contacting cells from lymphoma and normal cells with the agent, and after a period of time comparing the amount of bcl-6 nucleic acid in each sample, a difference indicating the effectiveness of the agent. The bcl-6 gene is a source of probes and primers, which are used to diagnose diffuse-type B cell lymphoma and B

CC cell lymphoma in a subject. Anti-Bcl-6 antibodies may also be used for  
 CC this purpose. The methods are useful for treating non-Hodgkin's lymphoma  
 XX  
 XX Sequence 706 AA;

Query Match 100.0%; Score 3793; DB 3; Length 706;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-284;  
 Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTRHSDVILNINRLSRDILTDVIVVSRGEPRAHKTVMACSGIFYSI 60  
 DB 1 MASPADSCIOFTRHSDVILNINRLSRDILTDVIVVSRGEPRAHKTVMACSGIFYSI 60  
 QY 61 FTDOUKCNLSVINLDEINBEGCILLDMYTSRLNLRGINIMAWATAMVLOMEHVDT 120  
 DB 61 FTDOUKCNLSVINLDEINBEGCILLDMYTSRLNLRGINIMAWATAMVLOMEHVDT 120  
 QY 121 CRKFTKASAEVNSAIKPPREFLNSRMLMPDIMAAYRGREVENNLPLRSAPGCSRAAF 180  
 DB 121 CRKFTKASAEVNSAIKPPREFLNSRMLMPDIMAAYRGREVENNLPLRSAPGCSRAAF 180  
 QY 181 APSLYSGLSTPPASYSMSYSHLPVSSLLFSDEEFDRVMVNPFPKERALPCDSAPVPVG 240  
 DB 181 APSLYSGLSTPPASYSMSYSHLPVSSLLFSDEEFDRVMVNPFPKERALPCDSAPVPVG 240  
 QY 241 EYSRPTLEVSPPVNCNSNITSPKETTPEARSMDHVSVAAGLKPAAASANAPFPDCDKAS 300  
 DB 241 EYSRPTLEVSPPVNCNSNITSPKETTPEARSMDHVSVAAGLKPAAASANAPFPDCDKAS 300  
 QY 301 KEERSSSEDEIALHFEPPNAPLNKRGIVSPQSDCQPNSPTEACSSKNACTIQASG 360  
 DB 301 KEERSSSEDEIALHFEPPNAPLNKRGIVSPQSDCQPNSPTEACSSKNACTIQASG 360  
 QY 361 SEPAPKPTDPKACNMKKYKFTVINSINQAKKPGQAEIGRLSPRAYTAPACOPMPER 420  
 DB 361 SEPAPKPTDPKACNMKKYKFTVINSINQAKKPGQAEIGRLSPRAYTAPACOPMPER 420  
 QY 421 ENMDLOSPTKLASGSDSTIPQASRLNINVRNMTGSSPSSSSSHPLVMHPKCTSCS 480  
 DB 421 ENMDLOSPTKLASGSDSTIPQASRLNINVRNMTGSSPSSSSSHPLVMHPKCTSCS 480  
 QY 481 OSPOHAEMLHTGPTFAEEMGTQSEYSDSCENGAFCNECDCFSEASLKRHTLT 540  
 DB 481 OSPOHAEMLHTGPTFAEEMGTQSEYSDSCENGAFCNECDCFSEASLKRHTLT 540  
 QY 541 HSDKPYKCDRCQASFPYKGNLASHKTVHGEKPYRCNICGAGFNRPANLKTHTRIHSGEK 600  
 DB 541 HSDKPYKCDRCQASFPYKGNLASHKTVHGEKPYRCNICGAGFNRPANLKTHTRIHSGEK 600  
 QY 601 PYKCEFCGARFVQVAHLRAHVLHTHGEKPYRCNICGAGFNRPANLKTHTRIHSGEK 660  
 DB 601 PYKCEFCGARFVQVAHLRAHVLHTHGEKPYRCNICGAGFNRPANLKTHTRIHSGEK 660  
 QY 661 EKCNLFPRHKSQRLRLRQKGAITNTKVQYVSATDLPPELPKAC 706  
 DB 661 EKCNLFPRHKSQRLRLRQKGAITNTKVQYVSATDLPPELPKAC 706

XX Homo sapiens.  
 OS US6140125-A.  
 XX 31-OCT-2000.  
 PD 15-OCT-1999; 99US-00418640.  
 XX 15-OCT-1999; 99US-00418640.  
 PF 15-OCT-1999; 99US-00418640.  
 XX 15-OCT-1999; 99US-00418640.  
 FR (ISIS-) ISIS PHARM INC.  
 XX Taylor JK, Cowseart LM;  
 PI WPI: 2001-048959/06.  
 DR N-PSDB; AAC81137.  
 XX  
 PS  
 XX  
 CC  
 CC This sequence represents human bcl-6. Bcl-6 (also known as B-cell  
 CC CLL/lymphoma 6, zinc finger protein 51 and LA23) is a sequence-specific  
 CC DNA-binding transcriptional repressor. The bcl-6 gene is expressed in  
 CC germinal centre B- and T-cells and is required for germinal centre  
 CC formation and Th-2 mediated antibody affinity maturation. Bcl-6 may also  
 CC play a role in the regulation of apoptosis. The bcl-6 gene is located on  
 CC chromosome 3q27, a region which undergoes a high frequency of  
 CC translocation events. Such chromosomal translocations can result in  
 CC aberrant forms of bcl-6, which are strongly implicated in the  
 CC pathogenesis of several types of lymphoma, and have also been reported in  
 CC acute lymphoblastic leukaemia and post-transplant lymphoproliferative  
 CC disorders. The invention relates to antisense oligonucleotides targeted  
 CC to the human bcl-6 gene, which inhibit its expression. A series of  
 CC oligonucleotides (AAC81144-C81223) were designed to target different  
 CC regions of the human bcl-6 mRNA, and were analysed for their effect on  
 CC bcl-6 mRNA levels by quantitative real-time PCR. The oligonucleotides of  
 CC the invention are useful for diagnosis, prevention and treatment of  
 CC conditions associated with aberrant forms of bcl-6, such as lymphomas,  
 CC acute lymphoblastic leukaemia and post-transplant lymphoproliferative  
 CC disorders  
 XX  
 XX Sequence 706 AA;  
 SQ  
 Query Match 100.0%; Score 3793; DB 4; Length 706;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-284;  
 Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 301 KEEBRSSEDEIALHFEPPNAPLNKGLVSPQSDCCPNSETEACSSKNACILQASG 360  
 QY 361 SPPAKSPDTPKACNMKKYKFTIVNSLNQNAKPGGPEQAEIGRLSPRAYTAPPAQPMER 420  
 Db 361 SPPAKSPDTPKACNMKKYKFTIVNSLNQNAKPGGPEQAEIGRLSPRAYTAPPAQPMER 420  
 QY 421 ENIDLOSPTKLSASGEDSTIPQASRLNNIVNRSWTGSPRSSSESHSLYMHPPKCTSCGS 480  
 Db 421 ENIDLOSPTKLSASGEDSTIPQASRLNNIVNRSWTGSPRSSSESHSLYMHPPKCTSCGS 480  
 QY 481 OSPQHAEMCHTAGPTFAEEMGETOSRYSDSCENGAFCNECDRCRSEASLKRHTLOT 540  
 Db 481 OSPQHAEMCHTAGPTFAEEMGETOSRYSDSCENGAFCNECDRCRSEASLKRHTLOT 540  
 QY 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYPCNICGAQFNRPANLKTHTRIHSGEK 600  
 Db 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYPCNICGAQFNRPANLKTHTRIHSGEK 600  
 QY 601 PYKCTCGARFVQVAHLRAHVLHTGKPYPCNICGTRFRHLQTLKSHLRHTGKPYHC 660  
 Db 601 PYKCTCGARFVQVAHLRAHVLHTGKPYPCNICGTRFRHLQTLKSHLRHTGKPYHC 660  
 QY 661 EKCMLHFRHKSQRLHLRQKHGALTNTKVOYRSATDLPPLPRAC 706  
 Db 661 EKCMLHFRHKSQRLHLRQKHGALTNTKVOYRSATDLPPLPRAC 706

RESULT 3

ADL82847  
 ID ADL82847 standard; protein: 706 AA.

AC ADL82847;

DT 17-JUN-2004 (first entry)

DE Human PRO26296, SEQ ID 49.

XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;  
 KW Antiallergic; Muscular; Neuroprotective; Nephrotoxic; Antiinflammatory;  
 KM Gene Therapy; PRO; B cell related disorder; cancer;  
 KW Immune-mediated inflammatory disease; human.

XX Homo sapiens.

OS WO2004024097-A2.

XX 25-MAR-2004.

XX 15-SEP-2003; 2003WO-US029097.

XX 16-SEP-2002; 2002US-0411392P.

XX (GETH ) GENENTECH INC.

XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI,  
 PI Wu TD;

XX WPI: 2004-329389/30.

XX N-PSDB; ADL82846.

XX New PRO polypeptide, useful for diagnosing and treating a B cell related  
 PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune  
 PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.

XX Claim 10; Fig 49; 695pp; English.

XX The present invention relates to PRO proteins and their coding sequences.  
 CC The PRO proteins are useful for diagnosing and treating a B cell related  
 CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polyasaccharide  
 CC antigen unresponsiveness, selective IGA deficiency, selective IGM  
 CC deficiency, selective deficiency of Igg subclasses, immunodeficiency with  
 CC hyper IGM, transient hypogammaglobulinemia of infancy, Burkitt's  
 CC lymphoma, intermediate lymphoma, follicular lymphoma, type II

CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic  
 CC anemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or  
 CC ankylosing spondylitis. The PRO proteins are also useful for preparing a  
 CC medicament for treating a condition that is responsive to the PRO  
 CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO  
 CC coding sequences are useful as hybridization probes in chromosome and  
 CC gene mapping, in preparing PRO proteins, or in generating transgenic  
 CC animals or knockout animals, which in turn are useful in the development  
 CC and screening of therapeutically useful reagents.

XX Sequence 706 AA;

Query Match 100.0%; Score 3793; DB 8; Length 706;

Best Local Similarity 100.0%; Pred. No. 9.8e-284;

Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTTHASDVLLNLRSLDITDVIVSREOFRAKTVLMACGLFYSI 60

Db 1 MASPADSCIOFTTHASDVLLNLRSLDITDVIVSREOFRAKTVLMACGLFYSI 60

QY 61 FTDLKCNLSVINLDEINPEGFCILLDFYTSRLNREGNIAVMAVTAMYLQMEHVDT 120

Db 61 FTDLKCNLSVINLDEINPEGFCILLDFYTSRLNREGNIAVMAVTAMYLQMEHVDT 120

QY 121 CRKFKASBAEMVSAIKPREEFPLNSRMLPQDIMA YRGREVENNLPLRSAPGCEBRAF 180

Db 121 CRKFKASBAEMVSAIKPREEFPLNSRMLPQDIMA YRGREVENNLPLRSAPGCEBRAF 180

QY 181 APSLSGLSTPPASYSYMYSHLYVSSLLFSDERFDVAMPVAPNPPKERRALPCDSARVPV 240

Db 181 APSLSGLSTPPASYSYMYSHLYVSSLLFSDERFDVAMPVAPNPPKERRALPCDSARVPV 240

QY 241 EYSRPTLEVPNVCNSNITYSPKETTIPBEASDMHYSAEGLKPAAPARAPYPCCKAS 300

Db 241 EYSRPTLEVPNVCNSNITYSPKETTIPBEASDMHYSAEGLKPAAPARAPYPCCKAS 300

QY 301 KEEBRSSEDEIALHFEPPNAPLNKGLVSPQSDCCPNSETEACSSKNACILQASG 360

Db 301 KEEBRSSEDEIALHFEPPNAPLNKGLVSPQSDCCPNSETEACSSKNACILQASG 360

QY 361 SPPAKSPDTPKACNMKKYKFTIVNSLNQNAKPGGPEQAEIGRLSPRAYTAPPAQPMER 420

Db 361 SPPAKSPDTPKACNMKKYKFTIVNSLNQNAKPGGPEQAEIGRLSPRAYTAPPAQPMER 420

QY 421 ENIDLOSPTKLSASGEDSTIPQASRLNNIVNRSWTGSPRSSSESHSLYMHPPKCTSCGS 480

Db 421 ENIDLOSPTKLSASGEDSTIPQASRLNNIVNRSWTGSPRSSSESHSLYMHPPKCTSCGS 480

QY 481 OSPQHAEMCHTAGPTFAEEMGETOSRYSDSCENGAFCNECDRCRSEASLKRHTLOT 540

Db 481 OSPQHAEMCHTAGPTFAEEMGETOSRYSDSCENGAFCNECDRCRSEASLKRHTLOT 540

QY 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYPCNICGAQFNRPANLKTHTRIHSGEK 600

Db 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTGKPYPCNICGAQFNRPANLKTHTRIHSGEK 600

QY 601 PYKCTCGARFVQVAHLRAHVLHTGKPYPCNICGTRFRHLQTLKSHLRHTGKPYHC 660

Db 601 PYKCTCGARFVQVAHLRAHVLHTGKPYPCNICGTRFRHLQTLKSHLRHTGKPYHC 660

QY 661 EKCMLHFRHKSQRLHLRQKHGALTNTKVOYRSATDLPPLPRAC 706

Db 661 EKCMLHFRHKSQRLHLRQKHGALTNTKVOYRSATDLPPLPRAC 706

RESULT 4

ADL14017  
 ID ADL14017 standard; protein: 706 AA.

AC ADL14017;

DT 21-OCT-2004 (first entry)

DE Human NF-kappaB pathway-associated protein SeqID18.  
 XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;  
 XX antiarthritic; antirheumatic; gastrointestinal-gen; antiaesthetic;  
 XX antileishmaniasis; immunomodulator; cerebroprotective; vasotropic;  
 XX immunosuppressive; vulnary; gene therapy; immune disorder;  
 XX inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;  
 XX hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;  
 XX hyper-igm syndrome; hypodidrotic ectodermal dysplasia;  
 XX X-linked anhidrotic ectodermal dysplasia; immunodeficiency;  
 XX viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV, influenza;  
 XX viral replication; host cell survival; evasion of immune response;  
 XX rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;  
 XX atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;  
 XX autoimmune disorder; hyper immune activity;  
 XX aberrant acute phase response; hypercongenital condition; birth defect;  
 XX necrotic lesion; wound; organ transplant rejection;  
 XX aberrant signal transduction; proliferating disorder; cancer;  
 XX HIV propagation; human.  
 XX Homo sapiens.  
 XX MO2004065577-A2.  
 XX 05-AUG-2004.  
 XX 13-JUN-2004; 2004MO-US000798.  
 XX PF 14-JAN-2003; 2003US-0440068P.  
 XX PR 12-MAY-2003; 2003US-0469757P.  
 XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX PI Nadler SG, Neubauer MG, Feder JN, Carman J,  
 XX DR MPI; 2004-562168/54.  
 XX N-PDB; ADR14016.  
 XX PT New isolated polynucleotides and polypeptides associated with NF-kappaB  
 XX pathway, useful for diagnosing, treating, or preventing disorders or  
 XX diseases associated with NF-kappaB pathway.  
 XX PS Claim 6; SEQ ID NO 18; 237pp; English.  
 XX This invention relates to the novel association of protein sequences (and  
 XX the genes which encode them) to the NF-kappaB pathway. The invention may  
 XX be useful for the production of compounds with an antiinflammatory,  
 XX cytostatic, hepatotropic, virucide, antiaesthetic, antirheumatic,  
 XX gastrointestinal-gen, antiaesthetic, antiaesthetic, antirheumatic,  
 XX immunomodulator, cerebroprotective, vasotropic, immunosuppressive or  
 XX vulnary activity or for gene therapy. The proteins and nucleotides are  
 XX useful for diagnosing, preventing, treating, or ameliorating conditions  
 XX or diseases associated with the NF-kappaB pathway. The condition is an  
 XX immune disorder, an inflammatory disorder, an inflammatory disorder  
 XX related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,  
 XX hepatic disorders, Hodgkin's lymphoma, haematopoietic tumours, hyper-igm  
 XX syndromes, hypodidrotic ectodermal dysplasia, X-linked anhidrotic  
 XX ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,  
 XX hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell  
 XX survival, evasion of immune responses, rheumatoid arthritis, inflammatory  
 XX bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick  
 XX syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper  
 XX immune activity, disorders related to aberrant acute phase responses,  
 XX hypercongenital conditions, birth defects, necrotic lesions, wounds,  
 XX organ transplant rejection, conditions related to organ transplant  
 XX rejection, disorders related to aberrant signal transduction,  
 XX proliferating disorders, cancers and HIV propagation in cells infected  
 XX with other viruses. The present sequence is that of a human protein which  
 XX is subject to the novel association with the NF-kappaB pathway of the  
 XX invention. Note: This sequence does not appear in the specification but  
 XX was obtained by the indexer from Genbank.

Query Match 100.0%; Score 3793; DB 8; Length 706;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-264;  
 Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MASPADSCIOPTFRHSDVILNLRSRDILDDVIVVSRQOPRAKTVLMAQGLFYSI 60  
 1 MASPADSCIOPTFRHSDVILNLRSRDILDDVIVVSRQOPRAKTVLMAQGLFYSI 60  
 61 FTDQKCNLSVINLDPETINPBGFCILDPMTYSLNLRBGNIMAVMATMTYOMEHVDT 120  
 61 FTDQKCNLSVINLDPETINPBGFCILDPMTYSLNLRBGNIMAVMATMTYOMEHVDT 120  
 61 FTDQKCNLSVINLDPETINPBGFCILDPMTYSLNLRBGNIMAVMATMTYOMEHVDT 120  
 121 CKKFKTASAEVNSAIKPRESEFLNSRMIPDIDIMAYGREYVENNPLRSAGCESRAF 180  
 121 CKKFKTASAEVNSAIKPRESEFLNSRMIPDIDIMAYGREYVENNPLRSAGCESRAF 180  
 121 CKKFKTASAEVNSAIKPRESEFLNSRMIPDIDIMAYGREYVENNPLRSAGCESRAF 180  
 181 ABSLYSGLSTPPASYSMTSHLPSVSSLLPSDEEFDRVMPVAMPFKERALPCDSARPVG 240  
 181 ABSLYSGLSTPPASYSMTSHLPSVSSLLPSDEEFDRVMPVAMPFKERALPCDSARPVG 240  
 181 ABSLYSGLSTPPASYSMTSHLPSVSSLLPSDEEFDRVMPVAMPFKERALPCDSARPVG 240  
 241 EYSRPTLEVSINVCHSNITSPKETTPEARSDMHTSVAGLKPAAPSARNAPYPCDKAS 300  
 241 EYSRPTLEVSINVCHSNITSPKETTPEARSDMHTSVAGLKPAAPSARNAPYPCDKAS 300  
 241 EYSRPTLEVSINVCHSNITSPKETTPEARSDMHTSVAGLKPAAPSARNAPYPCDKAS 300  
 301 KEERPSSEDELTALHPBPNAFLNRKGLVSPQSPKSDCQPSPTBACSSKACILQASG 360  
 301 KEERPSSEDELTALHPBPNAFLNRKGLVSPQSPKSDCQPSPTBACSSKACILQASG 360  
 301 KEERPSSEDELTALHPBPNAFLNRKGLVSPQSPKSDCQPSPTBACSSKACILQASG 360  
 361 SPPAKSPDTPKACNNKXKXFIYVNSLQNAKQGEQOAGLSPRAYTAPACQPMMP 420  
 361 SPPAKSPDTPKACNNKXKXFIYVNSLQNAKQGEQOAGLSPRAYTAPACQPMMP 420  
 361 SPPAKSPDTPKACNNKXKXFIYVNSLQNAKQGEQOAGLSPRAYTAPACQPMMP 420  
 421 ENLIDLOSPYKLSASGEDSTIPQASRLNITVNSMTGSPSSSSBSPLTMHPKCTSCS 480  
 421 ENLIDLOSPYKLSASGEDSTIPQASRLNITVNSMTGSPSSSSBSPLTMHPKCTSCS 480  
 421 ENLIDLOSPYKLSASGEDSTIPQASRLNITVNSMTGSPSSSSBSPLTMHPKCTSCS 480  
 481 OSPOHAEMLTAGPTFAEMGETOSEYSDSCENGAFPCNDFSEASIKRHTLTOT 540  
 481 OSPOHAEMLTAGPTFAEMGETOSEYSDSCENGAFPCNDFSEASIKRHTLTOT 540  
 481 OSPOHAEMLTAGPTFAEMGETOSEYSDSCENGAFPCNDFSEASIKRHTLTOT 540  
 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTEGKPYRCNLCGAOPNRPANLKTHTIRHSGEK 600  
 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTEGKPYRCNLCGAOPNRPANLKTHTIRHSGEK 600  
 541 HSDKPYKCDRCQASFRYKGNLASHKTVHTEGKPYRCNLCGAOPNRPANLKTHTIRHSGEK 600  
 601 PYKCECTGARFQVAHLRAHVLITGKPYPCICGTRPRRHQTLKSHIRHTGKPYHC 660  
 601 PYKCECTGARFQVAHLRAHVLITGKPYPCICGTRPRRHQTLKSHIRHTGKPYHC 660  
 601 PYKCECTGARFQVAHLRAHVLITGKPYPCICGTRPRRHQTLKSHIRHTGKPYHC 660  
 661 EKCNIHFRHKSQRLRLRKHQAINTTKQYVVSATDLPPELPAK 706  
 661 EKCNIHFRHKSQRLRLRKHQAINTTKQYVVSATDLPPELPAK 706  
 661 EKCNIHFRHKSQRLRLRKHQAINTTKQYVVSATDLPPELPAK 706  
 RESULT 5  
 ID ADY19590 standard; protein; 706 AA.  
 XX ADY19590;  
 XX ADY19590;  
 XX 05-MAY-2005 (first entry)  
 XX PRO polypeptide SEQ ID NO 5396.  
 XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
 XX Antirheumatic; Antiaesthetic; Osteopathic; Hemoclastic; Antiaemic;  
 XX Antihydroic; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;  
 XX Virucide; Gastrointestinal-Gen.; Antiprotic; Antiaesthetic;  
 XX Antiallergic; diagnosis.  
 XX Homo sapiens.  
 XX MO2005016962-A2.

XX 24-FEB-2005.  
XX 11-AUG-2004; 2004MO-US026249.  
XX 11-AUG-2003; 2003US-0493546P.  
XX (GETH ) GENENTECH INC.  
XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;  
XX WPI; 2005-182330/19.  
XX  
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and  
XX treating an immune related disorder, e.g. systemic lupus erythematosus,  
XX rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.  
XX  
XX Claim 8; SEQ ID NO 5396; 158bp; English.  
XX  
XX The invention relates to an isolated nucleic acid encoding a PRO  
XX polypeptide. The polypeptide, agonist or an antagonist, antibody,  
XX composition, and method are useful for diagnosing and treating an immune  
XX related disorder, e.g. systemic lupus erythematosus, rheumatoid  
XX arthritis. The present sequence represents a PRO polypeptide.  
XX  
XX Sequence 706 AA;  
SQ  
Query Match 100.0%; Score 3793; DB 9; Length 706;  
Best Local Similarity 100.0%; Pred. No. 9.8e-284;  
Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MASPADSCIOPTTRASDVLTNLRSDILTDVIVVSREOPRAKTVLMACGGLFYSI 60  
DB 1 MASPADSCIOPTTRASDVLTNLRSDILTDVIVVSREOPRAKTVLMACGGLFYSI 60  
QY 61 FTDLKCNLYINADPEINPBGFCILDFMTSRLNREGIMVMTAMTLOMEHVDT 120  
DB 61 FTDLKCNLYINADPEINPBGFCILDFMTSRLNREGIMVMTAMTLOMEHVDT 120  
QY 121 CRKTKASEAMVSAIKPREEPFNSRLMPQDMAVREVENNLPLRSGPCESEAF 180  
DB 121 CRKTKASEAMVSAIKPREEPFNSRLMPQDMAVREVENNLPLRSGPCESEAF 180  
QY 181 APSLYSGISTPPASYSMTSHLPVSSLLFSDPEFDVMPVNPPEKRALPCDSARPVG 240  
DB 181 APSLYSGISTPPASYSMTSHLPVSSLLFSDPEFDVMPVNPPEKRALPCDSARPVG 240  
QY 241 EYSRPTLEVSBNVCHSNISPEKETIPERASDMHYVAEGIKPAAPARNAYPFPCDKAS 300  
DB 241 EYSRPTLEVSBNVCHSNISPEKETIPERASDMHYVAEGIKPAAPARNAYPFPCDKAS 300  
QY 301 KEERRPSEDEITAHFEPPNAPLNKGIVSPOSKOCOPNSPEACSSNACILQASG 360  
DB 301 KEERRPSEDEITAHFEPPNAPLNKGIVSPOSKOCOPNSPEACSSNACILQASG 360  
QY 361 SPPAKSPDPKACWKYKFTIVINSINQNAKPGEGEQAELRLSPRAYTAPACOPPEP 420  
DB 361 SPPAKSPDPKACWKYKFTIVINSINQNAKPGEGEQAELRLSPRAYTAPACOPPEP 420  
QY 421 ENLDIQSPFKLSASGEDSTIPQASHLNINVRSMTGSPRSSSESHPLYMHPKCTGCS 480  
DB 421 ENLDIQSPFKLSASGEDSTIPQASHLNINVRSMTGSPRSSSESHPLYMHPKCTGCS 480  
QY 481 OSPHAEWCHTAGTFAEMGEQOSEXSDSCENGAFPCNCDRFESEBSLKHHTQT 540  
DB 481 OSPHAEWCHTAGTFAEMGEQOSEXSDSCENGAFPCNCDRFESEBSLKHHTQT 540  
QY 541 HSDKPKCDRCQASFRYKGNLASHKTIVTGEKPYRCNIGQAFNRPANILKTHRIHSEK 600  
DB 541 HSDKPKCDRCQASFRYKGNLASHKTIVTGEKPYRCNIGQAFNRPANILKTHRIHSEK 600  
QY 601 PYKCTGARFVQVAHLRAHVLITGEXRYPCEICTGTRPHILQTLKSHRLITGEXRPHC 660  
DB 601 PYKCTGARFVQVAHLRAHVLITGEXRYPCEICTGTRPHILQTLKSHRLITGEXRPHC 660

DB 601 PYKCTGARFVQVAHLRAHVLITGEXRYPCEICTGTRPHILQTLKSHRLITGEXRPHC 660  
QY 661 EKNLHFRKHSQRLRLRKHGAIITTKVOYRNSATDLPPELPKAC 706  
DB 661 EKNLHFRKHSQRLRLRKHGAIITTKVOYRNSATDLPPELPKAC 706  
RESULT 6  
ADRI4065  
ID ADRI4065 standard; protein; 706 AA.  
XX  
XX ADRI4065;  
XX  
XX 21-OCT-2004 (first entry)  
XX  
XX Human NF-kappaB pathway-associated protein Seq1066.  
XX  
XX NF-kappaB pathway; antiinflammatory; cytosolic; hepatotropic; vitruclide;  
XX antiarthritic; antirheumatic; gastrointestinal-Gen; antiaesthetic;  
XX antiarteriosclerotic; immunomodulator; cerebroprotective; vasotrophic;  
XX immunosuppressive; vitruclide; gene therapy; immune disorder;  
XX inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;  
XX hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;  
XX hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;  
XX X-linked; antihidrotic ectodermal dysplasia; immunodeficiency;  
XX viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;  
XX viral replication; host cell survival; evasion of immune response;  
XX rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;  
XX atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;  
XX autoimmune disorder; hyper immune activity;  
XX aberrant acute phase response; hypercongenital condition; birth defect;  
XX necrotic lesion; wound; organ transplant rejection;  
XX aberrant signal transduction; proliferating disorder; cancer;  
XX HIV propagation; human.  
XX  
XX Homo sapiens.  
XX  
XX WO2004065577-A2.  
XX  
XX 05-AUG-2004.  
XX  
XX 13-JAN-2004; 2004MO-US000798.  
XX  
XX 14-JAN-2003; 2003US-0440068P.  
XX 12-MAY-2003; 2003US-0469757P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
XX Nadler SG, Neubauer MG, Feder JN, Carman J;  
XX WPI; 2004-562168/54.  
XX  
XX N-PSDB; ADRI4064.  
XX  
XX New isolated polynucleotides and polypeptides associated with NF-kappaB  
XX pathway, useful for diagnosing, treating, or preventing disorders or  
XX diseases associated with NF-kappaB pathway.  
XX  
XX Claim 6; SEQ ID NO 66; 237bp; English.  
XX  
XX This invention relates to the novel association of protein sequences (and  
XX the genes which encode them) to the NF-kappaB pathway. The invention may  
XX be useful for the production of compounds with an antiinflammatory,  
XX cytosolic, hepatotropic, vitruclide, antiaesthetic, antirheumatic,  
XX gastrointestinal-Gen, antiaesthetic, antiarteriosclerotic,  
XX immunomodulator, cerebroprotective, vasotrophic, immunosuppressive or  
XX vitruclide activity or for gene therapy. The proteins and nucleotides are  
XX useful for diagnosing, preventing, treating, or ameliorating conditions  
XX or diseases associated with the NF-kappaB pathway. The condition is an  
XX immune disorder, an inflammatory disorder, an inflammatory disorder  
XX related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,  
XX hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM  
XX syndrome, hypohidrotic ectodermal dysplasia, X-linked antihidrotic  
XX ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,

CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell  
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory  
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick  
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper  
 CC immune activity, disorders related to aberrant acute phase responses,  
 CC hyecongenital conditions, birth defects, necrotic lesions, wounds,  
 CC organ transplant rejection, conditions related to organ transplant  
 CC rejection, disorders related to aberrant signal transduction  
 CC proliferating disorders, cancers and HIV propagation in cells infected  
 CC with other viruses. The present sequence is that of a human protein which  
 CC is subject to the novel association with the NF-kappaB pathway of the  
 CC invention. Note: This sequence does not appear in the specification but  
 CC was obtained by the indexer from Genbank.

XX Sequence 706 AA;

Query Match 99.6%; Score 3777; DB 8; Length 706;  
 Best Local Similarity 99.6%; Pred. No. 1.7e-282;  
 Matches 703; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTRHASDVLLNLRSLRDILTDVVIIVSRQFRAHKTIVLMACSGLFYSI 60  
 DB 1 MASPADSCIOFTRHASDVLLNLRSLRDILTDVVIIVSRQFRAHKTIVLMACSGLFYSI 60  
 QY 61 FTDQKCNLSVINLDEINPEGFCILLDFMYTSRLNLRGNIMAVATMYLQMEHVDT 120  
 DB 61 FTDQKCNLSVINLDEINPEGFCILLDFMYTSRLNLRGNIMAVATMYLQMEHVDT 120  
 QY 121 CRKFKASAEAWVSATKPREBEFLNSRLMPDIDIMAYRGVEYNNLPLRSAPGCSRA 180  
 DB 121 CRKFKASAEAWVSATKPREBEFLNSRLMPDIDIMAYRGVEYNNLPLRSAPGCSRA 180  
 QY 181 APSLYSGLTSTPPASYSMTSLPVSSLLFSDEBRDVMPANPPKRALPCDSAPVP 240  
 DB 181 APSLYSGLTSTPPASYSMTSLPVSSLLFSDEBRDVMPANPPKRALPCDSAPVP 240  
 QY 241 EYSRPTLEVPNVCHSNITSPKETTIPBEARSMDHYSVAGLKPAAASARNAFP 300  
 DB 241 EYSRPTLEVPNVCHSNITSPKETTIPBEARSMDHYSVAGLKPAAASARNAFP 300  
 QY 301 KEERPSSEDEIALHFEPPNAPLNKGLVSPQSKDCQPNSTPTEACSSKNA 360  
 DB 301 KEERPSSEDEIALHFEPPNAPLNKGLVSPQSKDCQPNSTPTEACSSKNA 360  
 QY 361 SPPAKSTPTDPAKCMWKYKFTIVNSLNQAKPGPEOAEIGRLSPRAYTAPPA 420  
 DB 361 SPPAKSTPTDPAKCMWKYKFTIVNSLNQAKPGPEOAEIGRLSPRAYTAPPA 420  
 QY 421 ENLDLQSPKLSASGEDETIPOASRLNNIVNRSMTGSPRSSSHSPLVMHPPK 480  
 DB 421 ENLDLQSPKLSASGEDETIPOASRLNNIVNRSMTGSPRSSSHSPLVMHPPK 480  
 QY 481 QSPHASMCLHTAGPTAEEMGETOSEYSDSCENGAFCNCECDCRSEBASLKR 540  
 DB 481 QSPHASMCLHTAGPTAEEMGETOSEYSDSCENGAFCNCECDCRSEBASLKR 540  
 QY 541 HSDKPYCDRCQASFRYKGNLASHKTVHTGKPYRNCICGAQFNRPANLKT 600  
 DB 541 HSDKPYCDRCQASFRYKGNLASHKTVHTGKPYRNCICGAQFNRPANLKT 600  
 QY 601 PYKCTGAPRVQVAHRAHVLHTGKPYRNCICGRFRHLOTLKSHLHTG 660  
 DB 601 PYKCTGAPRVQVAHRAHVLHTGKPYRNCICGRFRHLOTLKSHLHTG 660  
 QY 661 EKNLHFRHKSQALRLHROKGAITNTKVQYVSATDLPPELPKAC 706  
 DB 661 EKNLHFRHKSQALRLHROKGAITNTKVQYVSATDLPPELPKAC 706

RESULT 7  
 ADY15006  
 ID ADY15006 standard; protein; 706 AA.

AC ADY15006;  
 XX 05-MAY-2005 (first entry)  
 DT PRO polypeptide SEQ ID NO 812.

DE Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
 XX Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;  
 KW Antithyroid; Antidiabetic; Nephrotoxic; CNS-Gen.; Hepatocrotic;  
 KW Virucide; Gastrointestinal Gen.; Antipsoriatic; Antiaesthetic;  
 KW Antiallergic; ds; gene; diagnosis.

OS Homo sapiens.

XX WO2005016962-A2.

XX 24-FEB-2005.

XX 11-AUG-2004; 2004WO-US026249.

XX 11-AUG-2003; 2003US-0493546P.

XX (GETH ) GENENTECH INC.

XX Abbae A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX MPI; 2005-182330/19.

PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and  
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,  
 XX rheumatoid arthritis, osteoarthritis, chyloditis, or diabetes mellitus.

PS Claim 8; SEQ ID NO 812; 158bp; English.

CC The invention relates to an isolated nucleic acid encoding a PRO  
 CC polypeptide. The polypeptide, agonist or an antagonist, antibody,  
 CC composition, and method are useful for diagnosing and treating an immune  
 CC related disorder, e.g. systemic lupus erythematosus, rheumatoid  
 CC arthritis. The present sequence represents a DNA encoding a PRO  
 CC polypeptide.

XX Sequence 706 AA;

Query Match 99.6%; Score 3777; DB 9; Length 706;  
 Best Local Similarity 99.6%; Pred. No. 1.7e-282;  
 Matches 703; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTRHASDVLLNLRSLRDILTDVVIIVSRQFRAHKTIVLMACSGLFYSI 60  
 DB 1 MASPADSCIOFTRHASDVLLNLRSLRDILTDVVIIVSRQFRAHKTIVLMACSGLFYSI 60  
 QY 61 FTDQKCNLSVINLDEINPEGFCILLDFMYTSRLNLRGNIMAVATMYLQMEHVDT 120  
 DB 61 FTDQKCNLSVINLDEINPEGFCILLDFMYTSRLNLRGNIMAVATMYLQMEHVDT 120  
 QY 121 CRKFKASAEAWVSATKPREBEFLNSRLMPDIDIMAYRGVEYNNLPLRSAPGCSRA 180  
 DB 121 CRKFKASAEAWVSATKPREBEFLNSRLMPDIDIMAYRGVEYNNLPLRSAPGCSRA 180  
 QY 181 APSLYSGLTSTPPASYSMTSLPVSSLLFSDEBRDVMPANPPKRALPCDSAPVP 240  
 DB 181 APSLYSGLTSTPPASYSMTSLPVSSLLFSDEBRDVMPANPPKRALPCDSAPVP 240  
 QY 241 EYSRPTLEVPNVCHSNITSPKETTIPBEARSMDHYSVAGLKPAAASARNAFP 300  
 DB 241 EYSRPTLEVPNVCHSNITSPKETTIPBEARSMDHYSVAGLKPAAASARNAFP 300  
 QY 301 KEERPSSEDEIALHFEPPNAPLNKGLVSPQSKDCQPNSTPTEACSSKNA 360  
 DB 301 KEERPSSEDEIALHFEPPNAPLNKGLVSPQSKDCQPNSTPTEACSSKNA 360  
 QY 361 SPPAKSTPTDPAKCMWKYKFTIVNSLNQAKPGPEOAEIGRLSPRAYTAPPA 420  
 DB 361 SPPAKSTPTDPAKCMWKYKFTIVNSLNQAKPGPEOAEIGRLSPRAYTAPPA 420

Db 361 SPKASPTDPAKACWKKYKFTVLSNLQNAKBPGEQAEIGRLSPRAYTAPPAQCPMP 420  
 Qy 421 ENLDLQSPYKLSASGEDSTIPQASRLNNIVNRSMTGSPRSSSESHSPLYMHPKCTSCGS 480  
 Db 421 ENLDLQSPYKLSASGEDSTIPQASRLNNIVNRSMTGSPRSSSESHSPLYMHPKCTSCGS 480  
 Qy 481 QSPQHAEMCLHTAGPTPAEKEGETQSYSPSSCENGAFCNCECCRSSEASLKRHTLOT 540  
 Db 481 QSPQHAEMCLHTAGPTPAEKEGETQSYSPSSCENGAFCNCECCRSSEASLKRHTLOT 540  
 Qy 541 HSDKPYKCDRCQASFRKGNLASHKTVHTGKPYPCICGTRFRHLQTLKSHLRHTHSEK 600  
 Db 541 HSDKPYKCDRCQASFRKGNLASHKTVHTGKPYPCICGTRFRHLQTLKSHLRHTHSEK 600  
 Qy 601 PYKCTCGARFVQVAHLRAHVLHTGKPYPCICGTRFRHLQTLKSHLRHTHSEK 660  
 Db 601 PYKCTCGARFVQVAHLRAHVLHTGKPYPCICGTRFRHLQTLKSHLRHTHSEK 660  
 Qy 661 EKCMLHFRHKSQRLHLRQKGAITNTKVQYRVASATDLPPELPKAC 706  
 Db 661 EKCMLHFRHKSQRLHLRQKGAITNTKVQYRVASATDLPPELPKAC 706

RESULT 8  
 ID ADJ70182 standard; protein, 706 AA.  
 XX ADJ70182;  
 Dt 06-MAY-2004 (first entry)  
 XX  
 Dd Human heart mitochondrial protein as a therapeutic target SegID1988.  
 XX  
 Km mitochondrial; human; screening assay; diabetes mellitus;  
 Km Huntington's disease; osteoarthritis;  
 Km Leber's hereditary optic neuropathy; LHON;  
 Km mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
 Km myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
 Km neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  
 Km osteopathic; ophthalmological; cytostatic.

XX Homo sapiens.  
 OS  
 XX  
 PN W02003087768-A2.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 04-APR-2003; 2003WO-US010870.  
 XX  
 PR 12-APR-2002; 2002US-0372843P.  
 PR 17-JUN-2002; 2002US-038987P.  
 PR 20-SEP-2002; 2002US-0412418P.  
 XX  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 XX  
 PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;  
 PI Warnock DE;  
 DR WPI; 2003-845369/78.  
 XX  
 Dd Identifying a mitochondrial target for drug screening assays and for  
 Pt treating diseases associated with altered mitochondrial function,  
 Pt comprises detecting a modified polypeptide in a sample and correlating  
 Pt with the disease.  
 XX  
 PS Claim 1; SEQ ID NO 1988; 180pp; English.  
 XX  
 CC This invention relates to novel mitochondrial targets that can be used  
 CC for therapeutic intervention in treating a disease associated with  
 CC altered mitochondrial function. Specifically, it refers to a method for  
 CC identifying proteins of the human heart mitochondrial proteome that are  
 CC useful for drug screening assays, as well as therapeutic targets. The

CC present invention describes a method for identifying such proteins that  
 CC can be used in the treatment of various diseases associated with altered  
 CC mitochondrial function including diabetes mellitus, Huntington's disease,  
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
 CC compositions have neuroprotective, nootropic, antidiabetic,  
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
 CC cytostatic activities. This polypeptide sequence is a human heart  
 CC mitochondrial protein of the invention.

XX  
 SQ Sequence 706 AA;  
 Query Match 99.4%; Score 3771; DB 7; Length 706;  
 Best Local Similarity 99.4%; Pred. No. 4.9e-282;  
 Matches 702; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MASPADSCIOPTRHASDVLTNLRSLRDLTDTVIVVSHRQFRAHKTIVMACSGLYSI 60  
 Db 1 MASPADSCIOPTRHASDVLTNLRSLRDLTDTVIVVSHRQFRAHKTIVMACSGLYSI 60  
 Qy 61 FTDQKCNLSVINLDEINDEGFCILDFMYTSLRLRSGNIMAVATANTYLOMEHVDT 120  
 Db 61 FTDQKCNLSVINLDEINDEGFCILDFMYTSLRLRSGNIMAVATANTYLOMEHVDT 120  
 Qy 121 CRKPTKASEAMVSAIKPRPEEFLNSRMLPQDIMAARGREVENNLPLSAPGCSRAF 180  
 Db 121 CRKPTKASEAMVSAIKPRPEEFLNSRMLPQDIMAARGREVENNLPLSAPGCSRAF 180  
 Qy 181 APSLYSGLSTPPASYSWYSHLPVSSLLFSDDEFRDVAMPVANDPPEKRALPCDSARVP 240  
 Db 181 APSLYSGLSTPPASYSWYSHLPVSSLLFSDDEFRDVAMPVANDPPEKRALPCDSARVP 240  
 Qy 241 EYSRPTLEVPNVCHSNISYPPKETIPPEARSDMHSYVAGLKPAAPARNAPIYPCOKAS 300  
 Db 241 EYSRPTLEVPNVCHSNISYPPKETIPPEARSDMHSYVAGLKPAAPARNAPIYPCOKAS 300  
 Qy 301 KEERPSSEDEIALHFEPPNAPLNRKLVLPQSPQSKDCQPNSTFACSSKNACTILQASG 360  
 Db 301 KEERPSSEDEIALHFEPPNAPLNRKLVLPQSPQSKDCQPNSTFACSSKNACTILQASG 360  
 Qy 361 SPKASPTDPAKACWKKYKFTVLSNLQNAKBPGEQAEIGRLSPRAYTAPPAQCPMP 420  
 Db 361 SPKASPTDPAKACWKKYKFTVLSNLQNAKBPGEQAEIGRLSPRAYTAPPAQCPMP 420  
 Qy 421 ENLDLQSPYKLSASGEDSTIPQASRLNNIVNRSMTGSPRSSSESHSPLYMHPKCTSCGS 480  
 Db 421 ENLDLQSPYKLSASGEDSTIPQASRLNNIVNRSMTGSPRSSSESHSPLYMHPKCTSCGS 480  
 Qy 481 QSPQHAEMCLHTAGPTPAEKEGETQSYSPSSCENGAFCNCECCRSSEASLKRHTLOT 540  
 Db 481 QSPQHAEMCLHTAGPTPAEKEGETQSYSPSSCENGAFCNCECCRSSEASLKRHTLOT 540  
 Qy 541 HSDKPYKCDRCQASFRKGNLASHKTVHTGKPYPCICGTRFRHLQTLKSHLRHTHSEK 600  
 Db 541 HSDKPYKCDRCQASFRKGNLASHKTVHTGKPYPCICGTRFRHLQTLKSHLRHTHSEK 600  
 Qy 601 PYKCTCGARFVQVAHLRAHVLHTGKPYPCICGTRFRHLQTLKSHLRHTHSEK 660  
 Db 601 PYKCTCGARFVQVAHLRAHVLHTGKPYPCICGTRFRHLQTLKSHLRHTHSEK 660  
 Qy 661 EKCMLHFRHKSQRLHLRQKGAITNTKVQYRVASATDLPPELPKAC 706  
 Db 661 EKCMLHFRHKSQRLHLRQKGAITNTKVQYRVASATDLPPELPKAC 706

RESULT 9  
 AAR68743  
 ID AAR68743 standard; protein, 706 AA.  
 XX AAR68743;  
 AC AAR68743;  
 XX  
 Dt 25-MAR-2003 (revised)

DT 19-JUL-1995 (first entry)  
 XX BCL-6 zinc finger protein.  
 XX bcl-6 locus; non-Hodgkin lymphoma; B-cell lymphoma; B-lymphocyte;  
 KM diagnostic; therapeutic; chromosome-3q27; translocation; proto-oncogene;  
 KM diffuse large cell lymphoma; DCL; zinc finger.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Region 520..541  
 FT /label= Zinc-finger  
 FT Region 548..568  
 FT /label= Zinc-finger  
 FT Region 576..596  
 FT /label= Zinc-finger  
 FT Region 604..624  
 FT /label= Zinc-finger  
 FT Region 632..652  
 FT /label= Zinc-finger  
 FT Region 660..681  
 FT /label= Zinc-finger  
 XX  
 XX MO9429343-A1.  
 PD 22-DEC-1994.  
 XX  
 XX 09-JUN-1994; 94MO-US006669.  
 XX  
 XX 09-JUN-1993; 93US-00074967.  
 XX  
 PA (UYCO ) UNITV COLUMBIA NEW YORK.  
 PA (SLOK ) SLOAN KETTERING INST CANCER.  
 XX  
 PI Dalla-Favera R, Chaganti RS;  
 DR WPI; 1995-036403/05.  
 DR N-PSDB; AAQ68743.  
 XX  
 PT Nucleic acid from genetic locus bcl-6 - used to develop prods. for  
 PT diagnosis and therapy of B-cell lymphoma and non-Hodgkin's lymphoma.  
 XX  
 PS Disclosure; Page 90-94; 129pp; English.  
 XX  
 XX DNA was extd. from tumor tissue of 2 cases of IGH-producing diffuse-type  
 CC B-cell NHL carrying the t(3;14)(q27;q32) translocation. DNA analysis  
 CC showed that the breakpoints on 3q27 were located within 3 kb of the same  
 CC genomic locus, which was designated bcl-6. The human bcl-6 locus was  
 CC identified by screening a phage cDNA library constructed from B1ab B-cell  
 CC lymphoma mRNA. The zinc finger protein encoded by bcl-6 is given in  
 CC AAR68743. BCL-6 is a proto-oncogene specifically involved in the  
 CC pathogenesis of diffuse large cell lymphoma. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SO Sequence 706 AA:  
 Query Match 99.2%; Score 3763; DB 2; Length 706;  
 Best Local Similarity 99.3%; Pred. No. 2e-281;  
 Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTRHASNVLINLRSDILTDVIVVVSREOPRAHKTVMACSGFYST 60  
 DB 1 MASPADSCIOFTRHASNVLINLRSDILTDVIVVVSREOPRAHKTVMACSGFYST 60  
 QY 61 FTDLKCNLSVINLDPINPEGFCILDPMTYSRLNREGNIMAVMATATYLOMEHYVDT 120  
 DB 61 FTDLKCNLSVINLDPINPEGFCILDPMTYSRLNREGNIMAVMATATYLOMEHYVDT 120  
 QY 121 CRKIKASAEAMVSAIKPRPEEFNLSRLMPDIDIMAYRGREVENNLPLRSAPGCSERAF 180  
 DB 121 CRKIKASAEAMVSAIKPRPEEFNLSRLMPDIDIMAYRGREVENNLPLRSAPGCSERAF 180

QY 181 APSLYSGLSTPPASYSMTSHLPVSSLLRFDSEFRDVRMPVNPPEKRALPCDSARPVPG 240  
 DB 181 APSLYSGLSTPPASYSMTSHLPVSSLLRFDSEFRDVRMPVNPPEKRALPCDSARPVPG 240  
 QY 241 EYSRPTLEVSPNVCHSNITSPKETTPEARSDMHYSAVAGLKPAAPSARNAPYPCDAS 300  
 DB 241 EYSRPTLEVSPNVCHSNITSPKETTPEARSDMHYSAVAGLKPAAPSARNAPYPCDAS 300  
 QY 301 KEERPSSEDEIALHFEPPNAPLNKGLVSPSPKSCOPNSPTEACSSKACILQASG 360  
 DB 301 KEERPSSEDEIALHFEPPNAPLNKGLVSPSPKSCOPNSPTEACSSKACILQASG 360  
 QY 361 SPAPKPTDPKACMKKXKFFIVLSLNQNAKPGQEOALGRLSPRAYTAPACOPMEP 420  
 DB 361 SPAPKPTDPKACMKKXKFFIVLSLNQNAKPGQEOALGRLSPRAYTAPACOPMEP 420  
 QY 421 ENLDIQSPTKLSASGEDSTIPQASHLNNIVNRSMTGSRSSSESHSPLYMHPKCTSCGS 480  
 DB 421 ENLDIQSPTKLSASGEDSTIPQASHLNNIVNRSMTGSRSSSESHSPLYMHPKCTSCGS 480  
 QY 481 OSPOHAEMLHTAGPTFAEMGETOEXSDSCENGAFFCNECDRFSSEASLKHHTLOT 540  
 DB 481 OSPOHAEMLHTAGPTFAEMGETOEXSDSCENGAFFCNECDRFSSEASLKHHTLOT 540  
 QY 541 HSDKPYKCDRCQASFRYKGNLASHKTVAHTEKPYPCNICGAQPNRPAULKTHRJHSGEK 600  
 DB 541 HSDKPYKCDRCQASFRYKGNLASHKTVAHTEKPYPCNICGAQPNRPAULKTHRJHSGEK 600  
 QY 601 PYKCTCGARFVQVAHLRAVLHTEKPYPCNICGTRFRHLQTLKSHLRHTGKPYHC 660  
 DB 601 PYKCTCGARFVQVAHLRAVLHTEKPYPCNICGTRFRHLQTLKSHLRHTGKPYHC 660  
 QY 661 EKCNLHFRHKSQRLRLRQKGAITNTKYQVVSATDLPPELPKAC 706  
 DB 661 EKCNLHFRHKSQRLRLRQKGAITNTKYQVVSATDLPPELPKAC 706

RESULT 10  
 ID AAY78792 standard; protein; 706 AA.  
 AC AAY78792;  
 XX  
 DT 19-MAY-2000 (first entry)  
 XX  
 XX Human BCL-6 protein sequence.  
 XX  
 XX Bcl-6; human; B-cell lymphoma; regulator; non-Hodgkin's lymphoma;  
 KM diffuse type B-cell lymphoma.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 PN WO200000185-A1.  
 XX  
 PD 06-JAN-2000.  
 XX  
 PF 30-JUN-1999; 99WO-US014703.  
 XX  
 PR 30-JUN-1998; 98US-00107058.  
 XX  
 PA (UYCO ) UNITV COLUMBIA NEW YORK.  
 XX  
 PI Dalla-Favera R, Niu H;  
 XX  
 XX WPI; 2000-160631/14.  
 DR N-PSDB; AA290110.  
 PT Novel methods for regulating BCL-6 levels in cells used to treat humans  
 PT with lymphoma.  
 XX  
 XX Example; Fig 9, 159pp; English.  
 XX  
 CC This sequence represents the human bcl-6 protein sequence. The invention



CC relates to a vertebrate bcl-6 locus which is the breakpoint cluster  
 CC region in B-cell lymphomas, and contains a bcl-6 gene encoding a BCL-6  
 CC polypeptide. Administration of a molecule which induces phosphorylation  
 CC of BCL-6 and thereby induces BCL-6 degradation, can be used as a method  
 CC of regulating BCL-6 in cells. The methods of the invention can be used to  
 CC regulate, and especially to decrease BCL-6 levels in cells. The methods  
 CC may also be used to screen putative therapeutic agents for treatment of  
 CC non-Hodgkin's lymphoma, by contacting cells from lymphoma and normal of  
 CC bcl-6 nucleic acid in each sample, a difference indicating the amount of  
 CC effectiveness of the agent. The bcl-6 gene is a source of probes and  
 CC primers, which are used to diagnose diffuse-type B cell lymphoma and B  
 CC cell lymphoma in a subject. Anti-BCL-6 antibodies may also be used for  
 CC this purpose. The methods are useful for treating non-Hodgkin's lymphoma  
 CC  
 XX Sequence 706 AA:

Query Match 99.2%; Score 3763; DB 3; Length 706;  
 Best Local Similarity 99.3%; Pred. No. 2e-281;  
 Matches 701; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 MASPADSCIOFTRHASPVLINLNRLSRDILTDVVIIVSREOFRAHKTVMACSGLYYSI 60  
 1 MASPADSCIOFTRHARPVLINLNRLSRDILTDVVIIVSREOFRAHKTVMAMGGLYSI 60  
 61 FTDLKCNLSVINLDPINPEGFCILLDPYTSRLNREGNIMAVMTAMYLQMEHVVD 120  
 61 FTDLKCNLSVINLDPINPEGFCILLDPYTSRLNREGNIMAVMTAMYLQMEHVVD 120  
 121 CRKRTKASEAMVSAICPREEFLNSRLMPODIMAARGREVENNNPLRSAPCESRAF 180  
 121 CRKRTKASEAMVSAICPREEFLNSRLMPODIMAARGREVENNNPLRSAPCESRAF 180  
 121 CRKRTKASEAMVSAICPREEFLNSRLMPODIMAARGREVENNNPLRSAPCESRAF 180  
 181 APSLISGLSTPPASYSMTSHLPSVSLFSDERFDVMPVAPPKERRALPCDSARVP 240  
 181 APSLISGLSTPPASYSMTSHLPSVSLFSDERFDVMPVAPPKERRALPCDSARVP 240  
 241 EYSRPTLEVPNCHSNISPKETIPERASDMHYSAEGIKPAAPSARNAFPCCDKAS 300  
 241 EYSRPTLEVPNCHSNISPKETIPERASDMHYSAEGIKPAAPSARNAFPCCDKAS 300  
 301 KEERPSSEDEIALHFEPPNAPLRKGLVSPQSKDCONSSTECSSNACILQASG 360  
 301 KEERPSSEDEIALHFEPPNAPLRKGLVSPQSKDCONSSTECSSNACILQASG 360  
 361 SPPKSTDPKACNWKYKFTVINSLNOMAKGPEOAEIGRLSPRAYTAPACOPMEP 420  
 361 SPPKSTDPKACNWKYKFTVINSLNOMAKGPEOAEIGRLSPRAYTAPACOPMEP 420  
 361 SPPKSTDPKACNWKYKFTVINSLNOMAKGPEOAEIGRLSPRAYTAPACOPMEP 420  
 421 ENLDLQSPYTKLASGSDSTIPQASRLNNIVNRSMTGSPRSSBSHSPLYMHPKCTSCG 480  
 421 ENLDLQSPYTKLASGSDSTIPQASRLNNIVNRSMTGSPRSSBSHSPLYMHPKCTSCG 480  
 481 QSPHAEMLCHTAGPTAEEMGETQSEYSDSSCENAFECNECCRCRSEESLKRHTLOT 540  
 481 QSPHAEMLCHTAGPTAEEMGETQSEYSDSSCENAFECNECCRCRSEESLKRHTLOT 540  
 541 HSDPYKCDRCQASFRKYNLASHKTYHTGKPYRCNCGAOPNRPALKTHTIHSGEK 600  
 541 HSDPYKCDRCQASFRKYNLASHKTYHTGKPYRCNCGAOPNRPALKTHTIHSGEK 600  
 601 PYKCTGAPRVQVAHLIAHVLITGKPYRCICGTFRHLQTLKSHLHTGSKPYHC 660  
 601 PYKCTGAPRVQVAHLIAHVLITGKPYRCICGTFRHLQTLKSHLHTGSKPYHC 660  
 661 EKNLHFRHKSQRLHLRQKGAITNTKYQVRVATDLPRLPRAC 706  
 661 EKNLHFRHKSQRLHLRQKGAITNTKYQVRVATDLPRLPRAC 706

RESULT 11  
 ABB57289 standard; protein; 707 AA.

XX ABB57289;  
 AC 07-MAR-2002 (first entry)  
 DT Mouse ischaemic condition related protein sequence SEQ ID NO:814.  
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:814.  
 KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease.  
 XX Mus musculus.  
 XX WO200108188-A2.  
 XX 22-NOV-2001.  
 XX 18-MAY-2001; 2001WO-JP004192.  
 XX 18-MAY-2000; 2000JP-00145977.  
 XX (UNIT-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
 XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
 XX WPI; 2002-034733/04.  
 XX N-PSDB; AB199745.  
 XX Examining the ischaemic condition (e.g. occlusive ischaemia) by measuring  
 PT expression levels of particular genes defined in the specification or by  
 PT determining the expression profile of a gene group comprising these  
 PT genes.  
 XX Claim 2; Page 2004-2007; 2690JP; English.  
 PS The present invention describes a method for examining ischaemic  
 CC conditions, comprising measuring the expression levels of particular  
 CC genes (I) in a test sample or determining the expression profile of a  
 CC gene group in the sample comprising genes selected from (I). The method  
 CC is useful for examining the ischaemic condition (e.g. compressive  
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring  
 CC expression levels of particular genes (AB199912 to AB199914, encoding the  
 CC protein sequences in ABB57020 to ABB57174) or by determining the  
 CC expression profile of a gene group comprising these genes. The expression  
 CC levels or expression profiles produced by these genes are used as an  
 CC indicator when screening for ischaemic condition-improving drugs or  
 CC therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR  
 CC primers for a mouse ischaemic condition related sequence, which are used  
 CC in the exemplification of the present invention  
 XX  
 XX Sequence 707 AA;  
 Query Match 95.0%; Score 3602.5; DB 5; Length 707;  
 Best Local Similarity 94.2%; Pred. No. 5e-269;  
 Matches 666; Conservative 14; Mismatches 26; Indels 1; Gaps 1;

1 MASPADSCIOFTRHASPVLINLNRLSRDILTDVVIIVSREOFRAHKTVMACSGLYYSI 60  
 1 MASPADSCIOFTRHASPVLINLNRLSRDILTDVVIIVSREOFRAHKTVMACSGLYYSI 60  
 61 FTDLKCNLSVINLDPINPEGFCILLDPYTSRLNREGNIMAVMTAMYLQMEHVVD 120  
 61 FTDLKCNLSVINLDPINPEGFCILLDPYTSRLNREGNIMAVMTAMYLQMEHVVD 120  
 121 CRKRTKASEAMVSAICPREEFLNSRLMPODIMAARGREVENNNPLRSAPCESRAF 180  
 121 CRKRTKASEAMVSAICPREEFLNSRLMPODIMAARGREVENNNPLRSAPCESRAF 180  
 181 APSLISGLSTPPASYSMTSHLPSVSLFSDERFDVMPVAPPKERRALPCDSARVP 240  
 181 APSLISGLSTPPASYSMTSHLPSVSLFSDERFDVMPVAPPKERRALPCDSARVP 240  
 240 GEYSRPTLEVPNCHSNISPKETIPERASDMHYSAEGIKPAAPSARNAFPCCDKA 299

Db 241 NEYSRAMEVSPSLCHSNITVSPKAVPEBARSDIHVSDEGPKAVPARNAPFPCDKA 300  
Qy 300 SKEEERSSSEDEALHFEPPNAPLNKGI VSPQSPKSCCOPNSPPEACSSNACIQAS 359  
Db 301 SKEEERSSSEDEALHFEPPNAPLNKGI VSPQSPKSCCOPNSPPEACSSNACIQAS 360  
Qy 360 GSPAPSPDPKACNMKKYKFIYVNSLGNAPKQGEQOALRLSPRATAPACOPPME 419  
Db 361 GSPAPSPDPKACNMKKYKFIYVNSLGNAPKQGEQOALRLSPRATAPACOPPME 420  
Qy 420 PENLDIQSPKASGSDSTIPQASRLNINVRSMTGSPPSSSSHPLYMHPKCTSCG 479  
Db 421 PAULDQSPKASGSDSTIPQASRLNINVRSMTGSPPSSSSHPLYMHPKCTSCG 480  
Qy 480 SGGPQAEMLHAGTTPAEKMEGTSEVSDSCENGAFCNCCDRFEASIKRHTIQ 539  
Db 481 SGGPQAEMLHAGTTPAEKMEGTSEVSDSCENGAFCNCCDRFEASIKRHTIQ 540  
Qy 540 THSDKPYKCDRCQASFRYKGNLASHKTVHTGEKPYKCNICGAQPNRPALIKTHRIHSGE 599  
Db 541 THSDKPYKCDRCQASFRYKGNLASHKTVHTGEKPYKCNICGAQPNRPALIKTHRIHSGE 600  
Qy 600 KPYKCTCGARFVQVAHLRAHVLHTGEKPYKCEIGTFRRLQTLKSHLRHTGKPYH 659  
Db 601 KPYKCTCGARFVQVAHLRAHVLHTGEKPYKCEIGTFRRLQTLKSHLRHTGKPYH 660  
Qy 660 CEKCNLHFRHKSQRLHARQKGAITNTKYQVVSATDLPBPLPKAC 706  
Db 661 CEKCNLHFRHKSQRLHARQKGAITNTKYQVVSATDLPBPLPKAC 707

## RESULT 12

ID ABM84710 standard; protein; 458 AA.

XX ABM84710;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:4959.

XX KM gene therapy; human diagnostic and therapeutic polynucleotide; dlthp.

XX OS Homo sapiens.

XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,  
PI Hartshorne TA, Suchorolski MT, Altus CM, Pites SJ, Elder LV,  
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP,  
PI Stevens CA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,  
PI Paralta CH, Anderson SB, Rioux P, Shen BJ, Wu MC, Stuve LI,  
PI Lagace RE, Spito PA, Stewart EA, Wingrove J, Velt UA, Kitton ES,  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,  
PI Patury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.  
XX N-PSDB; ACN43362.

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecule, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.

PS Claim 27; Page; 190pp; English.

CC The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dlthp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorders, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dlthp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germ-line  
CC gene therapy. The present sequence data represents a dlthp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

SQ Sequence 458 AA;

Query Match 30.5%; Score 1158.5; DB 8; Length 458;

Best Local Similarity 37.6%; Pred. No. 1.5e-80; Indels 277; Gaps 15;

Matches 268; Conservative 49; Mismatches 118

Qy 1 MASPA--DSCI-----QFTRHAGSDVLLNINRLSRDILTDVIVVVSREQPRAHKTVMACS 54  
Db 1 MGSPAPAGALGVAFETRRSHSDVGNLNLRLRGLITDVTLLVGGQPLRAKAVLACS 60  
Qy 55 GLFYISIFTDQKCNLSVINLDEINPEGFCIILDFTYTSRLNLRGNIMAVMATMYLQW 114  
Db 61 GFFYSIFRGAAGVDVLSLPGPARGAPALDIDMTYSRLSLPATAVAVLAATVYLQW 120  
Qy 115 EHVYDTCRKFTKASAEWVSAIKPRPEREINRMLMPQIMAYRREVENNLPJRSARG 174  
Db 121 EHVYQACHRFQAS----- 134  
Qy 175 CESRAFAPELVSGLSTPPASYSMYGHLPVSSLLFSDDEFRDVMFANPPEKRALPCDS 234  
Db 135 -----YEPFGIS----- 141  
Qy 235 ARPVGEYSRPTLEVSPVYCHSNITVSPKETTPEARSDMHWVAGLKPAPASARNAPYF 294  
Db 142 -----LAPPL----- 145  
Qy 295 PCDKASKEERSSSEDEALHFEPPNAPLNKGI VSPQSPKSCCOPNSPPEACSSNAC 354  
Db 146 -----EAEPT-----PPTAP-----PPGSPRSKGPDPPTSRG----- 176  
Qy 355 ILQASGPPAKSPDTPKACNMKKYKFIYVNSLGNAPKQGEQOALRLSPRATAPACOPPME 401  
Db 177 ---CSGGPPSPAPSPDKACNMKKYKFIYVNSLPGDEASSSSSSSSSEGGPIPGPOS 233  
Qy 402 RLSPRAYTAPPAQOPMEPENLDIQSPKASGSDSTIPQASRLNINVRSMTGSPPSS 461  
Db 234 RLSPTATVQFKGAP-----ASTPVLLTQAQDT-----SSGP----- 267  
Qy 462 SESHSPLYMHPKCTSCGSGSPQAHMCLHTAGPTFAEMGTOSGYSSSCENGAFCN 521  
Db 268 SEARAPL-----PGSBF-----FSCQ 283  
Qy 522 ECDRCSEASLKRHTLQTHSDPKYCDRCQASFRYKGNLASHKTVHTGEKPYKCNICGA 581  
Db 284 NCEAVAGSSGID-SLVPDEDEKPYKQUCRSSFRYKGNLASHKTVHTGEKPYKCNICGA 342  
Qy 582 OFNRPANLKTTHRIHSGEKPYKCTCGARFVQVAHLRAHVLHTGEKPYKCEIGTFRFH 641  
Db 343 RFRPAPANLKTTHRIHSGEKPYKCTCGARFVQVAHLRAHVLHTGEKPYKCEIGTFRFH 402  
Qy 642 LQTLKSHLRHTGKPYKCEKCNLHFRHKSQRLHARQKGAITNTKYQVVSATDLPBPLPKAC 693  
Db 403 LQTLKSHLRHTGKPYKCEKCNLHFRHKSQRLHARQKGAITNTKYVHI 454



PT dependent disease (e.g. breast cancer) comprises a nucleic acid sequence  
 PT that encodes the angiogenesis-associated antigen AAC2-1 or AAC2-2.

XX Claim 50, Page 57, 57pp, English.

XX The present invention relates to an expression vector for inducing an  
 CC anti-tumour immune response in a patient. Also provided is a method of  
 CC using such a vector to treat angiogenesis-dependent diseases. The  
 CC composition and methods are useful in diagnosing, preventing, prognosing  
 CC or treating an angiogenesis-dependent disease, preferably a breast  
 CC cancer. The DNA molecule and protein may also be used in drug screening  
 CC assays. The present invention is an AAC2 protein sequence shown in the  
 CC exemplification of the invention

XX Sequence 479 AA:

Query Match 30.5%; Score 1155; DB 7; Length 479;  
 Best Local Similarity 38.3%; Pred. No. 2,9e-80;  
 Matches 268; Conservative 58; Mismatches 142; Indels 232; Gaps 15;

QY 1 MASP--DSCI---QFTRASDVLTNMRSDLTITVVIVYSEOPRAHKTVMACS 54  
 DB 1 MGPAPREGALGYRRETRHSSDVLGNLMLRLGLITVTLVGGQPLRAHRAVLIAQS 60  
 QY 55 GLPYSIFTDQKCNLAVINDPEINPEFCILDFWYTSRLNREGNIMAVATAMYLQM 114  
 DB 61 GFPTYSIFRGRAGGVVLSLPGPEARGFAPLIDFMTYSLRLSPATAVLAATYLLQM 120  
 QY 115 EHVVDTCRKFKASAEAMVSAIKRPREEFNLSPMDIMAYRGREVENNLPLRSAPG 174  
 DB 121 EHVVAQCHRFQAS----- 134  
 QY 175 CEBRARAPLSLVSLSTPPASYSMYSHLPVSLLFSBEFRDVMVPANPPKRALPCDS 234  
 DB 135 -----YEPPLGIS----- 141  
 QY 235 ARPVPGEYSRPTLEVPVCHSNISYSPKETIPREARSDMHVSVAELKPAFARAPAYF 294  
 DB 142 ----- 145  
 QY 295 PCDKASKEERPSSEDEIALHFPNPAPLNRKGLVSPSPQSKDCQPNSPTEACSSKMAC 354  
 DB 146 -----EAPPT-----PPTAP-----PPGSPRRSEGHDPPTESRS----- 176  
 QY 355 ILQASGSPPAKSPTPDPKACNWKYKFTYVNSLQNAKPGPEBAELGRLSPRAYTPAPAC 414  
 DB 177 ---CSQGPSPAPSPDPKACNWKYKFTYVNSLQNAKPGPEBAELGRLSPRAYTPAPAC 223  
 QY 415 QPMBEPENLDLOSPTKLSAGEDSTIP-QASRLNINIVNSMTGSPSSSESHSPLYMHP 473  
 DB 224 QALRPSGDDEASSSSSSSSSESGPIPGPSRL-----SPTATVQF----- 265  
 QY 474 KCTSCGSPQSPQAHMCLHTAGPTFAEMGETOSEYSDSCENGAFPCNECDKPSSEASL 533  
 DB 266 ---KCG--APASTPYLLTSQ---AQTSGSPSERAPRLGSEBFSCQNECAVACSSGGL 316  
 QY 534 KRRTLTQHSKPYKCDRCQASFRYKGNLASHKTVHNGEYKRYCNICGAQNRANANKTHT 593  
 DB 317 D-SLVPEDEDKPYKCDRCSSFRYKGNLASHKTVHNGEYKRYCNICGAQNRANANKTHT 375  
 QY 594 RHSGEYKRYCETCGARFVVAHRAVHLHTGEKPYCEICGTRFPHLOTLTSHRIHT 653  
 DB 376 RHSGEYKRYCETCGARFVVAHRAVHLHTGEKPYCEICGTRFPHLOTLTSHRIHT 435  
 QY 654 GEKPYHCKCNLHFRHNSQURLHLRQNGAINTYKYQYRV 693  
 DB 436 GEKPYHCDPCGLHFRHNSQURLHLRQNGAINTYKYVYHI 475

RESULT 15  
 ADN38698  
 ID ADN38698 standard; protein; 479 AA.  
 XX

AC ADN38698;  
 XX 17-JUN-2004 (first entry)  
 XX

DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:16.

XX Human; differential expression; cancer; angiogenic disorder;  
 KW fibrotic disorder; psoriasis; ischemia; heart disease; atherosclerosis;  
 KW inflammatory disease; autoimmune disease;  
 KW retinal neovascularization syndrome; scarring; uterine fibroid;  
 KW detection; diagnosis; prognosis; drug screening; drug targeting;  
 KW wound healing; contraception; cytostatic; cardiac; immunomodulatory;  
 KW vulnerey; gene therapy; vaccine.

XX Homo sapiens.

PN WO2003042661-A2.

XX 22-MAY-2003.

PF 13-NOV-2002; 2002MO-US036810.

XX 13-NOV-2001; 2001US-0350666P.

PR 21-NOV-2001; 2001US-0332464P.

PR 29-NOV-2001; 2001US-0334393P.

PR 03-DEC-2001; 2001US-0335394P.

PR 14-DEC-2001; 2001US-0340376P.

PR 08-JAN-2002; 2002US-0347211P.

PR 10-JAN-2002; 2002US-0347349P.

PR 08-FEB-2002; 2002US-0355714P.

PR 13-FEB-2002; 2002US-0359077P.

PR 20-FEB-2002; 2002US-0368099P.

PR 29-MAR-2002; 2002US-0370110P.

PR 04-APR-2002; 2002US-0372246P.

PR 12-APR-2002; 2002US-0386614P.

PR 05-JUN-2002; 2002US-0396839P.

PR 16-JUL-2002; 2002US-0397775P.

PR 22-JUL-2002; 2002US-0397845P.

PR 09-SEP-2002; 2002US-0409450P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevez PA;

PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;

XX WPI; 2003-468649/44.

DR N-PSDB; ADN38697.

XX Determining the presence or absence of a pathological cell in a patient,

PT useful for diagnosing, prognosing or treating cancer, comprises detecting

PT a nucleic acid in a biological sample.

XX Claim 12; SEQ ID NO 16; 1385pp; English.

XX The invention relates to nucleic acids and proteins (ADN38698-ADN40064)  
 CC whose expression is upregulated or downregulated in specific cancers or  
 CC other diseases such as angiogenic or fibrotic disorders, and to methods  
 CC of determining the presence or absence of a pathological cell in a  
 CC patient by detecting a nucleic acid at least 80% identical to those of  
 CC the invention or by detecting a polypeptide of the invention. The  
 CC invention also relates to expression vectors and host cells comprising a  
 CC nucleic acid of the invention; antibodies which specifically bind a  
 CC polypeptide of the invention; use of such antibodies for drug targeting;  
 CC and methods of screening for modulators of activity or expression of the  
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
 CC antibodies and methods are useful for diagnosing, prognosing and treating  
 CC cancer and other conditions such as psoriasis, ischemia, heart disease,  
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
 CC neovascularization syndromes, scarring and uterine fibroids. They may  
 CC also be useful in wound healing and in contraception. The present  
 CC sequence represents a polypeptide of the invention.

Sequence 479 AA:

Query Match 30.5%; Score 1155; DB 7; Length 479;  
Best Local Similarity 38.3%; Pred. No. 2.9e-80;  
Matches 268; Conservative 58; Mismatches 142; Indels 232; Gaps 15;

QY	1	MASPA--DSCI-----QFTRIASDVLNLTNLRSDILTDVIVYSRQGFRAHKTVMACS	54
DB	1	MGSPAAEAGALGYVREFTRHSSDVLGNINELRLGILTDVTLVGGQPLRAHKAVALTACS	60
QY	55	GLFYSIPTDQKCNLAVINDPEINPEGFCLIDFMTSRNLREGINAMATAMYLQM	114
DB	61	GFTYISIRGAGVVDVLSLPGCEHARGFAPLIDFMTSRNLSPATAPAVLAATYLMQ	120
QY	115	EHVYDTCRKFIKASEAMVSAIKPREEFLNSRMLMPQDIMAYRGREVENNLELRSAFG	174
DB	121	EHVYQACHRFIQAS-----	134
QY	175	CESRAPAPSLYSGISTPPASYSMYSHLPVSSLLFSDDEFRDVMPVANPPKERRALPCDS	234
DB	135	-----YEPGIS-----	141
QY	235	ARPVGEYSRPTLEVSIVNCHSNISPKETIPBEARSDMYSAEGLKPAAPARNAPYF	294
DB	142	-----LRPL-----	145
QY	295	PCDKASKEERPSSEDEIALHFEPNAPLNKGLVSPQSPQSDQPNSPTEACSSKNAC	354
DB	146	-----EABPPT-----PPTAP-----PGSPRSEGHDPPTESRS-----	176
QY	355	ILQAGSPPAKSPPTDPACNMKKYKTYIVLSLNONAKPGPEQNELGRLSPRAYTAPAC	414
DB	177	-----CSQGPSPSPASDPKACNMKKYKTYIVLSN-----QASQAGSLVGERSSGQPCP	223
QY	415	QPMPEPNNLQSPPTXLSAGEDSTIP-QASRLNNIVNRSMWTSPPRSSBSHSPLYMHP	473
DB	224	QARLPSSDEASSSSSSSSSEEGPTIPGPOSRL-----SPTATVQF-----	265
QY	474	KTSCGSQSPOHAEMCLHTAGPTFAEMGETOSEYSDSCENGAFPCNECDCRPSEASL	533
DB	266	---KCG--APASTPYLLTSQ---AODTSGSPSERARLPGESEFFSCQNCCEAVAGCSGL	316
QY	534	KRHTLQTHSDKPYKCDRCQASFRYKGNLASHKTYVHTGKPYRCNICGAQFNRPANLKTHT	593
DB	317	D-SLVPGDEDEKPYCQLCRSSFRYKGNLASHKTYVHTGKPYRCNICGARFNRPANLKTHTS	375
QY	594	RIHSGEKPYKCECTGAPVVOVAHLRAVHLHTGKPYPCCEICGTRFRHLQTLKSHLRHT	653
DB	376	RIHSGEKPYKCECTGSRFVOVAHLRAVHLHTGKPYPCPTCGTRFRHLQTLKSHVRHT	435
QY	654	GEKPYHCEKNLHFRHKSQRLHLROKGAITNTKVOYRV	693
DB	436	GEKPYHCDPCGLHFRHKSQRLHLROKGAATNTKVNHI	475

Search completed: March 2, 2006, 03:49:45  
Job time : 192 secs

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GenCore version 5.1.7  
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**OM protein - nucleic search using genomeplus p2n model**

Run on: March 2, 2006, 00:18:39 ; Search time 9653 Seconds  
(without alignments)  
4157.410 Million cell updates/sec

Title: US-10-755-889-18

Sequence: 1 MASPADSCIOFTRHASPDL.....TKVQYRSATDLPPELPKAC 706

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

**Command line parameters:**

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-UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human40.cdi -LIST=45  
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**Database:**

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6: gb\_pat:\*  
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13: gb\_vt:\*  
14: gb\_ncg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	ID	Description
1	3793	100.0	3536	6 AR117606 Sequence
2	3793	100.0	3536	6 CS035889 Sequence
3	3793	100.0	3536	6 CS044841 Sequence

4	3793	100.0	3536	6 AR559323	AR559323 Sequence
5	3793	100.0	3536	6 AX410625	AX410625 Sequence
6	3793	100.0	3536	8 U00115	U00115 Human zinc-
7	3777	99.6	2499	8 HSZNFNPRA	HSZNFNPRA
8	3777	99.6	3630	6 CS031305	CS031305 Sequence
9	3777	99.6	3630	6 CS040257	CS040257 Sequence
10	3763	99.2	3720	6 AR142448	AR142448 Sequence
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12	3763	99.2	3720	6 AR577709	AR577709 Sequence
13	3750	98.9	2600	8 S67779	S67779 BCL5-CY82-H
14	3619	95.4	2067	6 CQ715154	CQ715154 Sequence
15	3617.5	95.4	4196	8 HSM807105	HSM807105 Sequence
16	3604.5	95.0	2210	9 MUSM6CL6	MUSM6CL6
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18	3602.5	95.0	2373	6 AX306062	AX306062 Sequence
19	3602.5	95.0	2373	9 MM041465	MM041465
20	3013	79.4	2634	5 AJ719545	AJ719545 Gallus ga
21	2585.5	68.2	4536	5 BC084912	BC084912 Xenopus 1
22	2565.5	67.4	4376	5 BC077915	BC077915 Xenopus 1
23	2314	61.0	125395	8 AC072022	AC072022 Homo sapi
24	2192	57.8	2277	5 BC059515	BC059515 Dario rer
25	2179	57.4	168505	14 AC080010	AC080010 Homo sapi
26	2151.5	56.7	196774	14 AC158397	AC158397 Mus muscu
27	2138.5	56.4	2112	5 AB197694	AB197694 Takifugu
28	2107	55.5	183575	14 AC152786	AC152786 Bos tauru
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31	1871	49.3	177883	14 CR847922	CR847922 Dario rer
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33	1851	48.8	211094	5 BX005335	BX005335 Zebrafish
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36	1157.5	30.5	3345	9 AB011665	AB011665 Mus muscu
37	1155	30.5	3345	6 CQ989655	CQ989655 Sequence
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40	1153.5	30.4	3595	8 BC059404	BC059404 Homo sapi
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43	1122.5	29.6	1749	6 AX255044	AX255044 Sequence
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**ALIGNMENTS**

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LOCUS AR117606 AR117606 3536 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 3 from patent US 6140125.  
ACCESSION AR117606  
VERSION AR117606.1 GI:14098512  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3536)  
AUTHORS Taylor,J.K. and Cowsett,L.M.  
TITLE Antisense inhibition of bcl-6 expression  
JOURNAL Patent: US 6140125-A 3 31-OCT-2000;  
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**ORIGIN**

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Score: 3793.00 Matches: 706  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: Gaps: 0

US-10-755-889-18 (1-706) x AR117606 (1-3536)

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QY 41 GluGlnPheArgAlaHISLysThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle 60  
DB 448 GAGCAGTTTGAACCCATAAAGCTTCATATGCTCGACGTGCGCTGTTCTATAGCATC 507  
QY 61 PheThrAaPILeUaenLysCysAenLeuSerValIleAenLeuAaPProGluIleAaPPro 80  
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QY 161 GluValValaGluAaenLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe 180  
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RESULT 2  
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LOCUS Sequence 5395 from Patent WO2005016962.  
DEFINITION CS035889  
ACCESSION CS035889.1 GI:60733752  
VERSION  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 Abbas, A., Clark, H., Ouyang, W., Williams, M. P., Wood, W. I. and Wu, T. D.  
AUTHORS Compositions and methods for the treatment of immune related  
TITLE diseases  
JOURNAL Patent: WO 2005016962-A 5395 24-FEB-2005;  
FEATURES  
SOURCE location/Qualifiers  
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Pred. No.: 3,896-135 Length: 3536  
Score: 3793.00 Matches: 706  
Percent Similarity: 100.0% Conservative: 0  
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DB: Gaps: 0  
US-10-755-889-18 (1-706) x CS035889 (1-3536)  
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VERSION CS044841.1 GI:61851389  
KEYWORDS Mus musculus (house mouse)  
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ORGANISM Mus musculus (house mouse)  
REFERENCE 1. Abbas, A., Clark, H., Ouyang, W., Williams, P. M., Wood, W. I. and Wu, T. D. Compositions and methods for the treatment of immune related diseases. Patent: WO 2005019258-A 5395 03-MAR-2005;  
JOURNAL Genentech, Inc. (US)  
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 VERSION AR559323.1 GI:53968739

KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 3536)  
 AUTHORS Horwitz, K.B. and Richter, J.  
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 Homidae; Homo.  
 REFERENCE  
 1 Alvarez, C., Horne, D., Perez-da-Silva, S. and Vockley, J. G.  
 AUTHORS Gene expression profiles in liver cancer  
 TITLE Patent: WO 0229103-A 3272 11-APR-2002;  
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 1 (bases 1 to 3536)  
 Ye,B.H., Iisra,F., Lo Coco,F., Knowles,D.M., Offit,K.,  
 Chaganti,R.S. and Dalla-Favera,R.  
 Alterations of a zinc finger-encoding gene, BCL-6, in diffuse  
 large-cell lymphoma

JOURNAL Science 262 (5134), 747-750 (1993)  
PUBMED 8235596  
REFERENCE 2 (bases 1 to 3536)  
AUTHORS Ye, B.H.  
TITLE Direct Submission  
JOURNAL Submitted (04-AUG-1993) Binhui Hilda Ye, Pathology, College of Physicians & Surgeons of Columbia University, 630 W168th Street, New York, NY 10032, USA

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ORIGIN

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VERSION Z21943.1 GI:297025			

KEYWORDS  
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AUTHORS  
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FEATURES  
SOURCE

1A2-3 gene; zinc finger protein.  
Homo sapiens (human).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Hominoidea; Homo.  
1 (bases 1 to 2499)  
KERCKHAERT, J. P., DEWEINDT, C., TILLY, H., QUIEF, S., LECOQ, G. and  
BAETARD, C.  
1A2-3, a novel zinc-finger encoding gene, is disrupted by recurrent  
chromosome 3q27 translocations in human lymphomas  
Nat. Genet. 5 (1), 66-70 (1993)  
8220427  
2 (bases 1 to 2499)  
KERCKHAERT, J. P.  
Direct Submission  
Submitted (02-MAR-1993) KERCKHAERT J. P., INSERM U.124, Molecular  
Onco-Hematology, Place de Verdun, LILLE CEDEX, FRANCE, 59045  
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601 ProTyrAryCyG1uThrCyG1yA1AryPheAryA1AryA1AryA1AryA1AryA1Ary 620  
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621 ValLeu11eA1AryG1yAryAryProTyrProCyAryG1u11eCyG1yThraAryPheAry 640  
1945 GTGCTTATCAGCTGTGTAAGAGCCCTTATCCCTGAAATCTGTGGACCGGTTCCG 2004  
641 H1AryG1uThrLeuArySerA1AryAryA1AryAryA1AryAryA1AryAryAryAry 660  
2005 CACCTTCAACCTTGAAGGCACTGCAATTCACACAGAGAGAAACCTTACATTT 2064  
661 GluAryCyAenAryAryAryAryAryAryAryAryAryAryAryAryAryAryAryAry 680  
2065 GAGAAATGTACCTGATTTCTGTCACAAAGCAAGCTGCACTTCACTTGGCCGAGAG 2124  
681 H1AryA1A1AryAryAryAryAryAryAryAryAryAryAryAryAryAryAryAry 700  
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2185 GAGCTCCCAAGCTGCTC 2202  
RESULT 8  
CS031305  
LOCUS CS031305 3630 bp DNA linear PAT 10-MAR-2005





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Db	2161	GCCCAAGTTCAACCGGCCAGCCCAACTGAAAAACCACTCGAATTCATCTCGAGAGAG	2220
Qy	601	ProTyrLeuYsCysGlyIleThrCysGlyValAlaArgPheValGlnValAlaHisIleuArgAlaHis	620
Db	2221	CCCAACAANTCGAAACCTCGGAGGCCAGATTGTACAGGTGGCCCACTTCGGCCCAT	2280
Qy	621	ValIleuIleHisThrGlyGluYsProTyrProCysGluIleCysGlyIleThrArgPheArg	640
Db	2281	GTGCTTATCCACACTGGTGAGAAACCCATCCCTGTGAATCTGTGGACCCCGTTCCG	2340
Qy	641	HisLeuGlnIleLeuYsSerHisLeuArgIleHisThrGlyGluYsProTyrHisCys	660
Db	2341	CACCTTCAGACTCTGGAAGAGCCACTCGGATTCACACAGGAGAAACCTTACCATGT	2400
Qy	661	GluYsCysAenLeuHisPheArgHisIlySerGlnLeuAlaGluHisIleuArgGluYs	680
Db	2401	GAGAAAGTGTACCTGCATTCCTCGACAAAAGCCAGCGCACTTCACTTGCGCAGAG	2460
Qy	681	HisGlyAlaIleThrAsnThrLeuValGlnIleTyrArgValSerAlaThrAspLeuProPro	700
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Qy	701	GluLeuProYsAlaCys	706
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DEFINITION	Sequence 811 from Patent WO2005019258.		linear
ACCESSION	CS040257		
VERSION	CS040257.1	GI:61848078	
KEYWORDS			
SOURCE			
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homnidae; Homo.		
REFERENCE			
AUTHORS	1 Abbas, A., Clark, H., Ouyang, W., Williams, P.M., Wood, W.I. and Wu, T.D.		
TITLE	Compositions and methods for the treatment of immune related diseases		
JOURNAL	Patent: WO 2005019258-A 811 03-MAR-2005;		
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Score:	3777.00	Matches:	703
Percent Similarity:	99.7%	Conservative:	1
Best Local Similarity:	99.6%	Mismatches:	2
Query Match:	99.6%	Indels:	0
DB:	6	Gaps:	0
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Qy	21	AsnLeuAanArgLeuArgSerArgAspIleLeuThrAspValValIleValValSerArg	40
Db	481	AACCTTAATCGTCTCCGAGTGAAGACATCTTGACTGATGATGTGTCAATGTGTGAGCCGT	540

QY	41	GIUGINPHEAAGLAHIAIETVETHTVAlaIleuMeCAlaCySeSerGIyLeuPheTYSeRIIE	60
Db	541	GAGCAGTTTAAAGCCCAATAAAACGCTCTCACTAGCCTCCAGTGGCCTGTCTATATGACATC	600
QY	61	PheThRaSPGInLeuLYsCyAaSnLeuSeRValIleAaSnLeuASPProGIuIlIeAaSPro	80
Db	601	TTTACAGACCAAGTTGAATGCAACTTATAGTGGATCAATCTTGATCTCGAGATCAACCTT	660
QY	81	GIUGIyPHeCySIIeLeuLeuASPheMeTYrThrSeRaRgLeuASPheLeuRgIUGIy	100
Db	661	GAGGATTTCTGCATCTCTCTGCACTTCATGACATCTCGGCTCAATTTGGCGGAAGGCGC	720
QY	101	AaNIleMeCAlaValMeCAlaThRaIaMeCTYrLeuGIImeCUIhIeValIaIAsPThR	120
Db	721	AACATCAAGAGCTGTATATGCCACCGGCTTATGACCTCGAGATGAGACATGTTTGTGACACT	780
QY	121	CysaRgLYsPheIIeLYaIaSeRGIuIaGIuMeCValSeRaIleLYaSPRoRaRg	140
Db	761	TGCCGGAAGTTTATTAAAGCCAGTGAACAGAGATGGTTTCTTGCCATCAAGCCTCTCGT	840
QY	141	GIUGIuPHeLeuAaSeRaRgMeCLeuMeCPRoGIaAPRIleMeCAlaTYrThRgIyAaG	160
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QY	161	GIUValIaIaGIuAaSnLeuPProLeuAaRgSeRaIaPProGIyCySGIuSeRaRgIaPHe	180
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QY	181	AlaPSeRSeLeuTYrSeRGIyLeuSeThRProProlaISeRYSeRMeTYrSeRHIa	200
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QY	241	GIuTYrSeRaRgPProThRLeuGIuValSeRProAaValCYaHIsSeRaNIleTYrSeR	260
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QY	261	ProLYSGIuThRIlePProGIuIaIaARgSeRaSPMeCHIsTYrSeRaIaIaGIUGIy	280
Db	1201	CCCAAGAAACATCCACAGAAGGACAGAACTGATATCAGTACAGTGTGGCTGAGGGGC	1260
QY	281	IeUySPProAlaIaIaPSeRSeRaIaARgAaNIaIaPProTYrPhePProCYaAPlySaIaSeR	300
Db	1261	CTCAAAACCTGCGCCCTCCACGCCGGAATGGCCCCCTACTTCCCTTGTAACAAGGCGCAC	1320
QY	301	LYSGIUGIUGIaRgPSeRSeRGIuAaSPGIuIleAlaIeUHIaPHeGIuPProPProAa	320
Db	1321	AAAGAAAGAAAGAACCTCTCTCTCGAAGATGAGATTGCCCTGCAATTCAGAGCCCCCAT	1380
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QY	361	SeSPProProlaIaLYSeSPRoThRaSPProLYSaIaCYaAaNIThRlySaIySYrLYsPHe	380
Db	1501	TCCCTCCAGCCAGAGGCCCCACTGACCCCAAGCCTTGCACTGGAAAGAAATCAAGTTTC	1560
QY	381	IIeValIeAaNISeRLeuAaNGIaAaNIaIaLYsPProGIyGIyPProGIuIaIaGIuLeu	400
Db	1561	ATCTGTCTCAACAGCTCTCAACAGAAATGCCAAACAGAGGGGCTGTAGCAGCGCTGAGCTG	1620
QY	401	GIyARgLeuSeSPRoARgIaTYrThRaIaPProProlaICYSGInPProPheMeCUIuPPro	420

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 Qy 461 SerSerGlnSerHisSerProLeuThrlMetHisProProlysCysThrlSerCysGlySer 480  
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 Qy 481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500  
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 Qy 561 LeuAlaSerHisIleThrlValHisThrGlyGluApsProThrlYSerCysGly 580  
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 DEFINITION ARI42448  
 ACCESSION ARI42448  
 VERSION ARI42448.1 GI:15102747  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 3720)  
 AUTHORS Chaganti,R.S.K. and Dalla-Favera,R.  
 TITLE Cloning and uses of the genetic locus BCL-6  
 JOURNAL Patent: US 6174997-A 1 16-JAN-2001;  
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 Qy 21 AsnLeuApsnAryleuArySerAryApsIleLeuThrlAryValIleValAlaSerAry 40  
 Db 388 AACCTTATGCTCTCCGAGTCCGAGATCGAGACATTTTACATGATTTGTCTTGTGAGCCCT 447  
 Qy 41 GlnGlnPheAryAlaHisIleThrlValLeuMetAlaCysSerGlyLeuPheThrlSerIle 60  
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 Qy 61 PheThrlApsnLeuAryCysApsnLeuSerValIleApsnLeuApsProGluIleApsPro 80  
 Db 508 TTTCACAGCAGGTTGAATCAACCTTATGATGATCATCTAGATCTGAGATCAACCTT 567  
 Qy 81 GlnGlyPheCysIleLeuApsPheMetThrlYSerAryleuApsnLeuAryGluGly 100  
 Db 568 GAGGATTTGCACTCTCTGAGACTTATGATACATCTCGGCTCAATTTGCGGAGAGGC 627  
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 Qy 121 CysAryPhePheIleAryAlaSerGluAryGluMetValSerAlaIleAryProAry 140  
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RESULT 11
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ACCESSION 149950
VERSION    149950.1 GI:2472170
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 3720)
AUTHORS   Dalla-Favera, R. and Chaganti, R.S.K.
TITLE      Cloning and uses of the genetic locus bcl-6
JOURNAL    Patent: US 5641672-A 1 24-JUN-1997;
FEATURES   Location/Qualifiers
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Alignment Scores:
Pred. No.:      5,636-134
Score:          3763.00
Percent Similarity: 99.4%
Best Local Similarity: 99.3%
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DB:             6
Gaps:           0

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Qy      21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValValIleValAlaSerArg 40
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Qy      41 GLInGLInPheArgAlaHisLYsThrValLeuMetAlaCYsSerGLYLeuPheTYrSerIle 60
Db      448 GAGCAGTTTGAAGCCCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 507
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 ACCESSION AR577709  
 VERSION AR577709.1 GI:56580344  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 3720)  
 AUTHORS Chaganti, R.S.K. and Dalla-Favera, R.  
 TITLE Cloning and uses of the genetic locus bcl-6  
 JOURNAL Patent: US 6783945-A, 131-Aug-2004;  
 The Trustees of Columbia University in the City of New York and  
 Sloan-Kettering Institute for Cancer Research, New York, NY  
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Query Match: 99.2% Indels: 0  
DB: 6 Gaps: 0  
US-10-755-889-18 (1-706) x AR577709 (1-3720)

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QY 41 GluGluPheArgAlaHisIleThrValLeuMetAlaCysSerGlyLeuPheTyrSerIle 60  
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## RESULT 13

LOCUS 567779 2600 bp mRNA linear PRI 13-Apr-2001  
DEFINITION BCL5=Cy2-His2 zinc-finger transcription factor [human, liver,  
mRNA, 2600 nt].

ACCESSION 567779  
VERSION 567779.1 GI:459372

## KEYWORDS

## SOURCE

ORGANISM Homo sapiens (human)

Homosapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

## REFERENCE

1 (bases 1 to 2600)  
Miki,T., Kawamata,N., Hirose,S. and Aoki,N.  
Gene involved in the 3q27 translocation associated with B-cell  
lymphoma, BCL5, encodes a Kruppel-like zinc-finger protein  
Blood 83 (1), 26-32 (1994)

## JOURNAL

PUBMED 8274740  
GenBank staff at the National Library of Medicine created this  
entry [NCBI gisbq 141975] from the original journal article.

## REMARK

Location/Qualifiers  
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sequence presented in paper contains a frameshift in the  
coding region"

misc\_feature

gene

ORIGIN

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US-10-755-889-18 (1-706) x 567779 (1-2600)

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DEFINITION Sequence 1088 from Patent WO02068579.  
ACCESSION CQ715154  
VERSION CQ715154.1 GI:42276011  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Hominidae; Homo.

REFERENCE  
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
TITLE Kites, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
JOURNAL Patent: WO 02068579-A 1088 06-SEP-2002;  
PE Corporation (NY) (US)  
FEATURES  
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ORIGIN

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Best Local Similarity: 96.74 Mismatches: 3  
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US-10-755-889-18 (1-706) x CQ715154 (1-2067)

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Qy 300 rLysGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAs 320  
Db 852 CAAGAAGAAAGAGAGACCTCTCGGAAGATGAGATTGCCCTGCAATTGAGACCCCAA 911



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cy	680	gHhAGVAlA11ePhrasnhrhryValGnryrAryValSeA1aThraspdeuprPr	700
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VERSION	BX649185.1	GI:34366430	
KEYWORDS			
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REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
CONSRPTM	1 (bases 1 to 4196)		
TITLE	Lauber,J., Bahr,A., Mewes,H.W., Weill,B., Amid,C., Osanger,A.,		
JOURNAL	Pobo,G., Han,M. and Wiemann,S.		
COMMENT	The German Human cDNA Consortium Direct Submission Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFP686M22130) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcententrum, Neuherweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/ Location/Qualifiers		
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Best Local Similarity:	96.24	Mismatches:	3
Query Match:	95.44	Indels:	23
DB:	8	Gaps:	1

US-10-755-889-18 (1-706) x HSM807105 (1-4196)

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 Db 1169 GAGCAGTTTGAACCCCATTAACGCTCTCATATGCGCTGCAGAT----- 1211  
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Search completed: March 2, 2006, 03:08:00  
Job time : 9697 secs

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: March 2, 2006, 00:17:59 ; Search time 1092 Seconds  
(without alignments)  
4308.858 Million cell updates/sec

Title: US-10-755-889-18

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Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	3793	100.0	3536	13	ADR14016 Human NF-

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6	3793	100.0	3536	12	ADY19589	Ady19589 DNA encod
7	3777	99.6	3537	14	ADL2846	Adl2846 Human PRO
8	3777	99.6	3630	14	ADY15005	Ady15005 DNA encod
9	3777	99.6	4506	14	ADBS3822	Adbs3822 Human pro
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38	3602.5	95.0	1440	10	ADP13839	Adp13839 AAC2-2 co
39	3602.5	95.0	1440	10	ADP13839	Adp13839 AAC2-2 co
40	3602.5	95.0	1440	10	ADP13839	Adp13839 AAC2-2 co
41	3602.5	95.0	1440	10	ADP13839	Adp13839 AAC2-2 co
42	3602.5	95.0	1440	10	ADP13839	Adp13839 AAC2-2 co
43	3602.5	95.0	1440	10	ADP13839	Adp13839 AAC2-2 co
44	3602.5	95.0	1440	10	ADP13839	Adp13839 AAC2-2 co
45	3602.5	95.0	1440	10	ADP13839	Adp13839 AAC2-2 co

#### ALIGNMENTS

RESULT 1	
ID	AAC81137 standard; cDNA; 3536 BP.
XX	AAC81137;
AC	
XX	
DT	23-FEB-2001 (first entry)
XX	
DE	Human bcl-6 CDNA.
XX	
KW	Human; bcl-6; transcriptional repressor; germinal centre formation;
KW	Th-2 mediated antibody affinity maturation; apoptosis regulator;
KW	chromosome 3q27; lymphoma; acute lymphoblastic leukaemia;
KW	post-transplant lymphoproliferative disorder; expression inhibition;
KW	antisense therapy; ss.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	CDS
FT	328..2448
FT	/*tag= a
FT	/product= "Human bcl-6"
FT	/function= "transcriptional repressor"
XX	
PN	US6140125-A.
XX	
PD	31-OCT-2000.
XX	

PF 15-OCT-1999; 99US-00418640.  
XX B-cell CLL/lymphoma 6, zinc finger protein 51 and IAZ3) is a sequence-  
PR 15-OCT-1999; 99US-00418640.  
XX (ISIS-) ISIS PHARM INC.  
PA Taylor JK, Cowseert LM;  
PI WPI; 2001-048959/06.  
XX P-PSDB; AAB29640.  
DR Antisense compounds which specifically hybridize with and inhibit human  
XX bcl-6 expression, useful for treating bcl-6 related disorders, and  
PT preventing or delaying inflammation or tumor formation.  
PS Claim 1; Col 45-52; 42pp; English.  
XX This sequence represents cDNA encoding human bcl-6. Bcl-6 (also known as  
CC B-cell CLL/lymphoma 6, zinc finger protein 51 and IAZ3) is a sequence-  
CC specific DNA-binding transcriptional repressor. The bcl-6 gene is  
CC expressed in germinal centre B- and T- cells and is required for germinal  
CC centre formation and Th-2 mediated antibody affinity maturation. Bcl-6  
CC may also play a role in the regulation of apoptosis. The bcl-6 gene is  
CC located on chromosome 3q27, a region which undergoes a high frequency of  
CC translocation events. Such chromosomal translocations can result in  
CC aberrant forms of bcl-6, which are strongly implicated in the  
CC pathogenesis of several types of lymphoma, and have also been reported in  
CC acute lymphoblastic leukaemia and post-transplant lymphoproliferative  
CC disorders. The invention relates to antisense oligonucleotides targeted  
CC to the human bcl-6 gene, which inhibit its expression. A series of  
CC oligonucleotides (AAC81144-C81223) were designed to target different  
CC regions of the human bcl-6 mRNA, and were analysed for their effect on  
CC bcl-6 mRNA levels by quantitative real-time PCR. The oligonucleotides of  
CC the invention are useful for diagnosis, prevention and treatment of  
CC conditions associated with aberrant forms of bcl-6, such as lymphomas,  
CC acute lymphoblastic leukaemia and post-transplant lymphoproliferative  
CC disorders  
SQ Sequence 3536 BP; 936 A; 943 C; 835 G; 822 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 1,4e-192 Length: 3536  
Score: 3793.00 Matches: 706  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
Gaps: 0  
  
US-10-755-889-18 (1-706) x AAC81137 (1-3536)  
QY 1 MetAlaSerProAlaAapSerCysIleGlnPheThrArgHisAlaSerAppValIleuLeu 20  
DB 328 ATGCCCTCCGCGGCTGACAGCTGTATCCAGTTCACCCGCATGCACTGATGTTCTTCTC 387  
QY 21 AsnIleuAsnArgLeuAysSerArgAspIleLeuThrAspValIleValIleValIleSerArg 40  
DB 388 AACCTTAATGCTCTCCGAGTCCAGACACTTGACTAATGTTGATGCTTTGAGACCGT 447  
QY 41 GluIlnPheArgAlaHisIleValThrValIleuMetAlaCysSerArgIleuPheTyrSerIle 60  
DB 448 GAGCAGTTTGAAGCCCAATAAAGGTCCTCATGCGCTGCAGTGGCTGTTCTATAGCATC 507  
QY 61 PheThrAspGlnLeuLeuValCysAsnIleuSerValIleAsnIleuAspProGlnIleAsnPro 80  
DB 508 TTTACACACCAAGTTGAATGCAACCTTATGATGATCAATCTAGATCTCTGAGATCAACCT 567  
QY 81 GluIlnIlePheCysIleLeuLeuAspPheMetCysThrSerArgLeuAsnIleuAspGlnGly 100  
DB 568 GAGGAGATTCGACATCTCTGACTTCAATGACATCTGCGCTCAATTTGCGGAGAGGC 627  
QY 101 AsnIleuMetAlaValMetAlaThrAlaMetTyrIleuGlnMetGlnIleValIleAspThr 120  
DB 628 AACATCATGCTGTGATGCGCACCGCTATGATCTGACATGAGATGAGCATGTTGTGACACT 687

QY 121 CysArgLysPheIleIleValAlaSerGlnAlaGluMetValSerAlaIleValSerProProArg 140  
DB 688 TCCCGAGAGTTTATTAAAGCCAGTGAAGCAGAGATGTTTCTGCCATCAAGCTCTCTGCT 747  
QY 141 GluIlnPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlnArg 160  
DB 748 GAAAGATTCCTCAACAGCCGAGTGTGATGCCCAAGCATCATGAGCTATGCGGAGTCTGCT 807  
QY 161 GluValValIleGluAsnAsnLeuProIleuArgSerAlaProGlnIleCysGlnSerArgAlaPhe 180  
DB 808 GAGGTGTGTGAAGAAACCTGCACTGAGAGACGCTCCGAGTGTGAGAGCAGACCTTT 867  
QY 181 AlaProSerLeuTyrSerArgIleuSerThrProProAlaSerTyrSerMetTyrSerHis 200  
DB 868 GCCCCAGCTTACATGAGTGGCTGTCCACACCGCAGCTCTTATTCATGATCAAGCCAC 927  
QY 201 LeuProValIleSerIleuLeuPheSerAspGlnIlnPheArgAspValArgMetProVal 220  
DB 928 CTCCTGTGACAGCTCTCTCTTCCGATGAGAGTTTCGGAGATGTCGGATGCTGTG 987  
QY 221 AlaAsnProPheProGlnIlnArgAlaIleuProCysAspSerAlaArgProValProGly 240  
DB 988 GCCAACCTTCCCAAGAGAGGCGCACTCCATGTGATGATGCCAGGCAAGTCTCTGCT 1047  
QY 241 GluTyrSerArgProThrIleuGlnIleValSerProAsnValCysHisSerAsnIleTyrSer 260  
DB 1048 GAGTACAGCCGCGCCACATTTGAGAGTGTCCCAATGTGTGCACAGAAATCTATTTCA 1107  
QY 261 ProLysGluThrIleProGlnIlnArgSerAspMetHisTyrSerValAlaGlnGly 280  
DB 1108 CCCAAGAAACATCCCAAGAGGACACCAAGATGATGATGATGATGATGATGATGATGATG 1167  
QY 281 LeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLysAlaSer 300  
DB 1168 CTCAAACCTGTCGCCCCCTCAGCCCAAGAAATGCCCTTACTTCTTGTGACAAAGCCAC 1227  
QY 301 LysGlnGlnIlnArgProSerSerGlnAspGlnIleAlaLeuHisPheGlnProProAsn 320  
DB 1228 AAGAGAAAGAGAGACCTCTCTCGAAGATGATGATGATGATGATGATGATGATGATGAT 1287  
QY 321 AlaProLeuAsnArgLysGlnIleuValSerProGlnIlnSerProGlnIlnSerAspCysGln 340  
DB 1288 GCAACCTTGAACCGGAAGGCTGTGTTAGTCCACAGAGCCCAAGAAATCTGATGCGCAG 1347  
QY 341 ProAsnSerProThrGlnIlnCysSerSerLysAsnAlaCysIleLeuGlnIlnSerGly 360  
DB 1348 CCCAACTCCGCCACAGAGGCTGACAGCAAGTAAGAAATGCTTCATCTCAGGCTCTTGC 1407  
QY 361 SerProProAlaLysSerProThrAspProLysAlaCysAsnTrpLysTyrLysPhe 380  
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QY 401 GlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProProMetGlnPro 420  
DB 1528 GGCCTGCTTCCCAAGAGCTTACAGGCCCCACCTGCTGCAAGCACCACCAAGAGAGCT 1587  
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QY 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlnSerProArgSer 460  
DB 1648 CCAAGAGCCAGCGGCTCATATAACATGTTTACAGTCCATGACGAGGCTCTCCCGCAGC 1707  
QY 461 SerSerGlnSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlnSer 480  
DB 1708 AGCAGAGAGAGCCATCACACATCTATGATGACCCCGAAGTGCAGTCTGCGGCTCT 1767



Db 448 GAGCATTTAGAGCCATAAAGCTCCTCATGCGCTGAGAGTGGCTGTTCTATAGCATC 507  
 Qy 61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80  
 Db 508 TTTCAGACACAGATTGAAATGCAACTTAGTGATCAATCTAGATCCTAGATCAACCTC 567  
 Qy 81 GluGluPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100  
 Db 568 GAGGAGTTCTGATCTCTGAGCTTCACTGATCACTCTGAGCTTATGGCGGAGGGC 627  
 Qy 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGlnIleValValAspThr 120  
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 Db 688 TGCCTGAGAGTTTATTAAGCCAGTGAAGCAGAGATGGTTCTGCCATCAAGCTCTCGT 747  
 Qy 141 GluGluPheLeuAsnSerArgMetLeuMetProGluAspIleMetAlaTyrArgGlyArg 160  
 Db 748 GAAAGATTCTCTCAACAGCCGAGATGCTGATGCCCCAGACATCATGGCTATCGGGTCTG 807  
 Qy 161 GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGlnSerArgAlaPhe 180  
 Db 808 GAGTGGTGAACAACCTGCCACTGAGAGGCGCCCTGGGTGAGAGCAGAGCTTT 867  
 Qy 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200  
 Db 868 GCGCCGAGCTGTACAGTGGCTGTGTCCACCGCCAGCCCTTATTCAGTACAGCCAC 927  
 Qy 201 LeuProAlaSerSerLeuLeuPheSerArgGluGluPheArgAspValArgMetProVal 220  
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 Db 1348 CCGAATCTGCGCCACAGAGGCTGCAAGCATGAATCTCTGCAATCTCCAGGCTTCCGCGC 1407  
 Qy 361 SerProProAlaLysSerProThrAspProLysAlaCysAsnTrpLysValTyrLysPhe 380  
 Db 1408 TCCCTCTCAGCCAGAGAGAGCCCACTGAGCCCAAGCCCTGCAACTGGAAGAAATACAAATTC 1467  
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 Db 1468 ATCGTGTCAACAGCCCTCAACAGAAATGCCAAACAGAGGGGCGCTGAGAGGCTGAGAGCTG 1527  
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 Db 1708 ACCAGCGAGGACCTCACTCACTTACATGACACCCCGAAATGACAGCTCGCGCTCT 1767  
 Qy 481 GlnSerProGlnHisAlaGlnMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500  
 Db 1768 CAGTCCCAACAGACATGACAGATGTGCTTCCACACCGCTGGCCCACTTCCGCTAGAG 1827  
 Qy 501 MetGlyGluThrGlnSerGluTyrSerAspSerSerCysGluAsnGlyAlaPhePheCys 520  
 Db 1828 ATGGGAGAGACCCAGCTGAGTACTCAATCTTACCTGAGAGACGAGGCTTCTTCTGCG 1887  
 Qy 521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540  
 Db 1888 AATGAGTGTGACTGCGCTTCTCTGAGAGGCTCTCACTCAAGAGCAGACCGCTGAGACC 1947  
 Qy 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560  
 Db 1948 CACAGTGAACAACTTACAGATGTGACCGCTCCAGGCTCTTCCGCTACAAAGGCAAC 2007  
 Qy 561 LeuAlaSerHisLysThrValHisThrGlyGluLysProTyrArgCysAsnIleCysGly 580  
 Db 2008 CTGCGCAGCCACAAGACCGTTCATACCGGTGAGAAACCTTATCGTGTGCAACATGTGTGG 2067  
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 Db 2428 GAGCTCCCAAGCGCTGC 2445

RESULT 3  
 ABN96774  
 ID ABN96774 standard; DNA; 3536 BP.  
 XX ABN96774;  
 AC  
 XX  
 DT 13-AUG-2002 (first entry)  
 XX  
 DE Gene #3272 used to diagnose liver cancer.  
 XX Gene; liver cancer; de; hepatocellular carcinoma; hepatotropic;



KW metastatic liver tumour; cytostatic; expression profile; disease state;  
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.  
 OS Homo sapiens.  
 PN MO200229103-A2.  
 XX 11-APR-2002.  
 PD 02-OCT-2001; 2001MO-US030589.  
 PF 02-OCT-2000; 2000US-0237054P.  
 PR (GENE-) GENE LOGIC INC.  
 PA Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;  
 PI WPI; 2002-426119/45.  
 DR  
 XX  
 XX  
 PT Diagnosing and detecting the progression of liver cancer, hepatocellular  
 PT carcinoma or metastatic liver tumor in a patient, involves detecting the  
 PT level of expression of two or more genes in a liver tissue sample.  
 PS Claim 1; SEQ ID NO 3272; 298bp; English.  
 XX  
 CC The invention relates to a novel method for diagnosing and detecting the  
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver  
 CC tumour in a patient, and differentiating metastatic liver cancer from  
 CC hepatocellular carcinoma in a patient, involving detecting the level of  
 CC expression of two or more genes represented in ABN93503-ABN97455 in a  
 CC tissue sample. The method of the invention has hepatocytic, and  
 CC cytoskeletal activity. The method is useful for diagnosing and detecting  
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic  
 CC liver carcinoma in a patient. The method is useful for identifying  
 CC expression profiles which serve as useful diagnostic markers as well as  
 CC markers that can be used to monitor disease states, disease progression,  
 CC drug toxicity, drug efficacy and drug metabolism. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 3536 BP; 936 A; 943 C; 835 G; 822 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.4e-192 Length: 3536  
 Score: 3793.00 Matches: 706  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: Gaps: 0  
 US-10-755-889-18 (1-706) x ABN96774 (1-3536)  
 QY 1 MetAlaSerProAlaIAspSerCysIleGlnPheThrArgHISAlaSerAspValIleuLeu 20  
 DB 328 ATGCGCTCGCGCGCTGACAGCTGTATCCAGTTCAACCCGCAATGCGAGATGTTCTTCTC 387  
 QY 21 AsnIleuAsnArgIleuArgSerArgAspIleuThrAspValIleValIleValIleSerArg 40  
 DB 388 AACCTTAATCGTCTCCGAGTGCAGACATCTTGACTGATGTTGTCATTGTTGTAAGCCGT 447  
 QY 41 GluGlnPheArgAlaHISIleValThrValIleuMetAlaCysSerGlyIleuPheTyrSerIle 60  
 DB 448 GAGCAGTTTAAGCCCATTAACGCTCTCAATGGCTTCAGTGGCTTTTCTATAGCATC 507  
 QY 61 PheThrAspGlnIleuLysCysAsnIleuSerValIleAsnIleuAspProGlnIleAsnPro 80  
 DB 508 TTACAGACCAAGTTTAAATGCAACTTATGATGATCAATCAATCAATCAATCAACCT 567  
 QY 81 GluGlyPheCysIleIleuLeuAspPheMetTyrThrSerArgIleuAsnIleuArgGlyIle 100  
 DB 568 GAGGATTCTGCATCTCTCGACTTCATGTAACATCTCGGCTCAATTTCGGGAGGAGC 627

QY 101 AsnIleuMetAlaValMetAlaThrIleMetTyrLeuGlnMetGlnHISValIleAspThr 120  
 DB 628 AACATCATGGCTTGTATGAGCCAGCTATATCTTCACTCAATGAGCATGTTGGACACT 687  
 QY 121 CysArgLysPheHISIleValIleSerGlyIleValIleMetValIleSerIleProArg 140  
 DB 688 TGCCGAGAGTTTATTAAGCCAGTGAAGCAGAGATGTTTCTGCCATCAAGCCTCTCGT 747  
 QY 141 GluGlnPheLeuAsnSerArgMetIleuMetProGlnAspIleMetAlaTyrArgGlyArg 160  
 DB 748 GAAGATTCTCTCAACGCGAGATGATGCCCCAAGACATCAATGAGCTTATCGAGGCTGT 807  
 QY 161 GluValIleGluAsnAsnIleuProLeuArgSerAlaProGlyCysGlnSerArgAlaPhe 180  
 DB 808 GAGTGTGAGAAACAACTTGCACATGAGAGGCCCCCTGGGTGTAGAGCAGACCTT 867  
 QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200  
 DB 868 GCCCCAGCCTGTACAGTGGCTGTCCACACCGCCAGCCTTATTCATGTACAGCCAC 927  
 QY 201 LeuProValSerSerIleuLeuPheSerArgGlyIleuPheArgAspValIleMetProVal 220  
 DB 928 CTCCTGTGACAGCCTCTCTCTCTCCAGATGAGAGATTTCGGATGTCCGATGCTGTG 987  
 QY 221 AlaAsnProPheProLysGluArgAlaLeuProCysAspSerAlaArgProValProGly 240  
 DB 988 GCCAACCTTCTCCCAAGGAGCGGCACTCCATGATGATGTCAGGCCAGCTCTGTGT 1047  
 QY 241 GluTyrSerArgProThrIleuGluValIleSerProAsnValCysHISerAsnIleTyrSer 260  
 DB 1048 GAGTACAGCGCGCGCTTGTGAGGTCTCCCAATGTGTGCCACAGCATATCTATTA 1107  
 QY 261 ProLysGluThrIleProGluGluAlaArgSerAspMetHisTyrSerValIleGlyIle 280  
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 QY 281 LeuIleuProAlaIleProSerAlaArgAsnAlaProTyrPheProCysAspLysAlaSer 300  
 DB 1168 CTCAACCTCTGCTCCCTCTAGCCGAAATGCCCCCTACTTCTCTGTGACAGGCGAGC 1227  
 QY 301 LysGluGluGluArgProSerSerGluAspGluIleAlaLeuHISpHeGluProProAsn 320  
 DB 1228 AAGAGAAAGAGAGACCTCTCTCGAAGATGAGATGCTCCGTGATTTGAGAGCCCAAT 1287  
 QY 321 AlaProLeuAsnArgLysGlyIleuValIleSerProGlnSerProGlnLysSerAspCysGln 340  
 DB 1288 GCACCCCTGAACGGAAGGCTGTGATGTCACAGAGCCGCCAGAAATCTGACTGCGAG 1347  
 QY 341 ProAsnSerProThrGluAlaCysSerSerLysAsnAlaCysIleIleuGlnIleSerGly 360  
 DB 1348 CCCAACTCGCCCAACAGGCGCTGACAGATGAGATCTGCACTTCAGGCTTCTGCGC 1407  
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 DB 1408 TCCCTCTCAAGCCAGAGCCCACTGACCCCAAGCCCTGCACTGAGAAATCAAGATTC 1467  
 QY 381 IleValIleuAsnSerIleuAsnGlnIleAsnAlaLysProGlyIleProGluGlnIleGluLeu 400  
 DB 1468 ATGCTGTCAACAGCTCAACAGAAATGCCAAACCAAGGAGGCTGTGAGAGGCTGAG 1527  
 QY 401 GlyArgLeuSerProAlaGlyIleTyrThrAlaProProAlaCysGlnProPheGluPro 420  
 DB 1528 GCGCGCTTTCCTCCACAGGCTTCAACGCGCCCACTGCTGCGCAGCCACCATGAGACCT 1587  
 QY 421 GluAsnIleuAspLeuGlnSerProThrLysLeuSerAlaSerGlyIleAspSerThrIle 440  
 DB 1588 GAGAACCTTGACTTCCAGTCCCAACCAAGCTGATGTCACGCGGAGAGACTCAACATC 1647  
 QY 441 ProGlnIleSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460  
 DB 1648 CCACAGACGAGCGGCTCAATTAACATGTTAAACAGTTCATGAGGCGCTCTCCCGCAGC 1707  
 QY 461 SerSerGlnSerHISerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480

DB 1708 AGCAGGAGAGGACCACTACCACTCTACATGCAACCCCGAAGGACAGCTCTCGGCTCT 1767  
QY 481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500  
DB 1768 CAGTCCCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1827  
QY 501 MetGlyGlnThrGlnSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 520  
DB 1828 ATGGAGAGAGCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1887  
QY 521 AsnGlyCysAspCysArgPheSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 540  
DB 1888 AATGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1947  
QY 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGln 560  
DB 1948 CACAGGTGACAAACCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2007  
QY 561 LeuAlaSerHisLysThrValHisThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 580  
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QY 581 AlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgLysHisSerGlnGlnGln 600  
DB 2068 GCCCAGTTCAACCGGCGCAGCCAACTGAAACCACTGAAATTCATCTGAGAGAGAG 2127  
QY 601 ProTyrLysCysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 620  
DB 2128 CCTCAAAATGCGAAACCTGCGAGCGAGCATTTGTACAGGTGCGCCACCTCGTCCCAT 2187  
QY 621 ValLeuLeuHisThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 640  
DB 2188 GTGCTTATCCACACTGTGATGAAAGCCCTTACCTGTGAAATCTGTGACCCCTTCGCG 2247  
QY 641 HisLeuGlnThrLysSerHisLysArgLysHisThrGlnGlnGlnGlnGlnGlnGlnGln 660  
DB 2248 CACCTTCAAGCTGGAAGACCACTGCGATCACAACAGAGAGAAACCTTTCATTTG 2307  
QY 661 GlnLysCysAsnLeuHisPheArgHisLysSerGlnLeuArgLysLeuHisLysArgGln 680  
DB 2308 GAGAGAGTGAACCTGCACTTCCGTCACAAAGCCAGCTGCGATTCCTGCGCCCGAAG 2367  
QY 681 HisGlyAlaLeuThrPheThrLysValGlnTyrArgAlaSerLysAlaThrAspLeuPro 700  
DB 2368 CATGGCCCATCAACCAACAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 2427  
QY 701 GlnLeuProLysAlaCys 706  
DB 2428 GAGCTCCCAAGCTGCG 2445

RESULT 4  
ID ADR14016 standard; DNA; 3536 BP.  
XX ADR14016;  
XX 21-OCT-2004 (first entry)  
XX Human NF-kappaB pathway-associated gene Segid17.  
DB NF-kappaB pathway; antiinflammatory; cytosolic; hepatotropic; vitruide;  
KW antiarthritic; antirheumatic; gastrointestinal-gen; antiaesthetic;  
KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;  
KW immunosuppressive; vulnerary; gene therapy; immune disorder;  
KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;  
KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;  
KW hyper-igm syndrome; hypohidrotic ectodermal dysplasia;  
KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;  
KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;  
KW rheumatoid arthritis; host cell survival; evasion of immune response;  
KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAB;

KW autoimmune disorder; hyper immune activity;  
KW aberrant acute phase response; hypercongenital condition; birth defect;  
KW necrotic lesion; wound; organ transplant rejection;  
KW aberrant signal transduction; proliferating disorder; cancer;  
KW HIV propagation; gene; ds; human.  
OS Homo sapiens.  
PN MO2004065577-A2.  
PD 05-AUG-2004.  
PF 13-JAN-2004; 2004WO-US000798.  
PR 14-JAN-2003; 2003US-0440068P.  
PR 12-MAY-2003; 2003US-0469757P.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PI Nadler SG, Neubauer MG, Feder JN, Carman J;  
XX WPI, 2004-562168/54.  
XX P-PSDB; ADR14017.  
PT New isolated polynucleotides and polypeptides associated with NF-kappaB  
DB pathway, useful for diagnosing, treating, or preventing disorders or  
PS diseases associated with NF-kappaB pathway.  
PS Claim 1, SEQ ID NO 17; 237bp; English.  
XX This invention relates to the novel association of protein sequences (and  
CC the genes which encode them) to the NF-kappaB pathway. The invention may  
CC be useful for the production of compounds with an antiinflammatory,  
CC cytosolic, hepatotropic, vitruide, antiaesthetic, antiatherosclerotic,  
CC gastrointestinal-gen, antiaesthetic, antiatherosclerotic,  
CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or  
CC vulnerary activity or for gene therapy. The proteins and nucleotides are  
CC useful for diagnosing, preventing, treating, or ameliorating conditions  
CC or diseases associated with the NF-kappaB pathway. The condition is an  
CC immune disorder, an inflammatory disorder, an inflammatory disorder  
CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,  
CC hepatic disorders, Hodgkin's lymphoma, haematopoietic tumours, hyper-igm  
CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic  
CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,  
CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell  
CC survival, evasion of immune response, rheumatoid arthritis, inflammatory  
CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick  
CC syndrome, stroke, EAB, autoimmune disorders, disorders related to hyper  
CC immune activity, disorders related to aberrant acute phase response,  
CC hypercongenital conditions, birth defects, necrotic lesions, wounds,  
CC organ transplant rejection, conditions related to organ transplant  
CC rejection, disorders related to aberrant signal transduction,  
CC proliferating disorders, cancers and HIV propagation in cells infected  
CC with other viruses. The present sequence is that of a human gene which is  
CC subject to the novel association with the NF-kappaB pathway of the  
CC invention. Note: This sequence does not appear in the specification but  
XX was obtained by the indexer from Genbank.  
XX Sequence 3536 BP; 936 A; 943 C; 835 G; 822 T; 0 U; 0 Other;  
SQ

Alignment Scores:  
Pred. No.: 1,4e-192 Length: 3536  
Score: 3793.00 Matches: 706  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: Gaps: 0

US-10-755-889-18 (1-706) x ADR14016 (1-3536)  
QY 1 MetAlaSerProAlaPheSerCysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 20  
DB 328 ATGGCTCCCGGCTGACAGCTGATCCAGTTCAACCCCGCAGTGCAGTATGTTCTTCTC 387

Qy	21	AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValIleValValSerArg	40
Dd	388	AACTTATATGCTCTCCGAGGTCGAGACATCTTGACTGATGTTCATTTGTTGAGCCGT	447
Qy	41	GlulInpHeArgAlaHilyeThrValLeuMetAlaCysSerGlyLeuPheTYrSerIle	60
Dd	448	GAGCAGTTTGAAGCCCATTAACCGGTCTTCATGAGCCCTGCAGTGGCCGTTCATTAGCATC	507
Qy	61	PheThrSerpGlnLeuLeuPheCysAsnLeuSerValIleAsnLeuAspProGluIleAspPro	80
Dd	508	TTTACAGACCAAGTTGAATGCAACCTTAGTGTGATCATCTAGATCCTGAGATCAACCT	567
Qy	81	GlulGlyPheCysIleLeuLeuAspPheMetTYrThrSerArgLeuAsnLeuArgGluGly	100
Dd	568	GAGGGAATTTGTCATCTCTCTGTAATTCATGACACATCTGGCTCAATTTGGGGAAGGC	627
Qy	101	AsnIleMetAlaValMetAlaThrAlaMetTYrLeuGlnMetGluHlySvalValAspThr	120
Dd	628	AACTCATGTGCTGATGATGGCCAGCGCATATGACTGCAGATGAGCATGTTGTGACACT	687
Qy	121	CysArgIysPheHilyeValAserGluAlaGluMetValSerAlaIleLysProProArg	140
Dd	688	TGCGGAAAGTTATTAAAGGCCAGAGGACAGAGATGTTCTCGCATCAAGCCCTCTCGT	747
Qy	141	GluGluPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTYrArgGlyArg	160
Dd	748	GAAAGATTTCTTCACAGCCGAGATCTGATGCCCCAAGACATCAAGGCTTATGGGAGTGT	807
Qy	161	GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe	180
Dd	808	GAGGTGTGGAGAACACTCTGCATGAGAGCCCTCGGTGTGAGAGCAGAGCCTTT	867
Qy	181	AlaProSerIleuTYrSerGlyLeuSerThrProProAlaSerTYrSerMetTYrSerHis	200
Dd	868	GCCCCACCTGTACAGTGAGGCTGTCCACACCGCAGAGCTCTTATTCCATGTACAGCCAC	927
Qy	201	LeuProValSerSerLeuLeuPheSerArgpGluGluPheArgAspValArgMetProVal	220
Dd	928	CTCCCTGTACAGAGCTCTCTCTTCCCATAGAGATTCGGAGATGCCGATGCCCTGTG	987
Qy	221	AlaAsnProPheProLysGluArgAlaLeuProCysAspSerAlaArgProValProGly	240
Dd	988	GCCAAACCTTCCCCAGAGAGGGGACATCCCATGTGATGTGCCAGGCCAGTCCCTGT	1047
Qy	241	GluTYrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTYrSer	260
Dd	1048	GAGTACAGCCGGCCGACATTTGGAGGTGTCCCCCATGTGTGCCACAGCAATATCATTTCA	1107
Qy	261	ProLysGluThrIleProGluGluAlaArgSerPheMetIleTYrSerValAlaGluGly	280
Dd	1108	CCCAAGGAACATCCAGAGAGGCAAGATGTATGTACTACATGATGAGTGGCTGAGAGGC	1167
Qy	281	LeuLysProAlaAlaProSerAlaArgAsnAlaProTYrPheProCysAspLysAlaSer	300
Dd	1168	CTCAAACTGTGCCCCCTCAGCCCGGAATGCCCTTCCCTTGACAAAGCCAGC	1227
Qy	301	LysGluGluGluArgProSerSerGlnAspGluIleAlaLeuHisPheGluProProAsn	320
Dd	1228	AAAGGAAGAGAGACCTCTCTCGGAAGTGAATGTGCCCTGTGATTTGAGACCCCCCAT	1287
Qy	321	AlaProLeuAsnArgLysGlyLeuValSerProGlnSerProGlnLysSerAspCysGln	340
Dd	1288	GACCCCTGAAACGGAGAGGTGTGGTTAGTCCACAGAGGCCCCCAAAATTCATGTCGAG	1347
Qy	341	ProAsnSerProThrGluAlaCysSerSerLysAsnAlaCysIleLeuGluAlaSerGly	360
Dd	1348	CCCAACTGCCCCACAGAGCCTGCAGCAGTAAAGATGCTGCATCTCCAGGCTTCTGAC	1407
Qy	361	SerProProAlaLysSerProThrAspProLysAlaCysAsnTrpLysIleTYrLysPhe	380
Dd	1408	TCCCTTCAGCCAGAGGCCCTCACTAACCCTCAAGGCTGTGACATGGAAAGAAATACAAATT	1466

QY	381	IIleValIleuMetSerLeuIleuAnGlnIleuAlaIleValProGlyValProGluGlnIleValIleuLeu	400
Db	1468	ATTCGTGCTCAACACCTCTCAACCGAATGGCCAAACCGAGGGAGCTTGAAGCGCTGAAGCTG	1527
QY	401	GIVArgLeuSerProAlaGAlaTYrThralaProProAlaCYsGlnProPromeGluPro	420
Db	1528	GGCGGCGCTTTCCACGAGCGCTTACAGCGGCCCACTGCTCGCCAGGCCACCATGGAGCCT	1587
QY	421	GluIleuLeuIleuLeuGlnSerProThrLYleuSerAlaSerGlyGluIleuSerThrIle	440
Db	1588	GAGAACCTTGACCTCCAGCTCCCCAACCAACCTGAAGTGTCCAGCGGGAGGACTCCACCATC	1647
QY	441	ProGlnAlaSerAlaArgLeuIleuAlaMetIleValAlaAspArgSerMetThrGlySerProArgSer	460
Db	1648	CCACAAGCGACCGGCTCATTAACATGATTAAACAGTTCACAGTTCACAGCGGAGCTCTCCCGCAGC	1707
QY	461	SerSerGlnSerHisSerProLeuTYrMetHisProProLYsCYsThrSerCYsGlySer	480
Db	1708	AGCAGCGAGACCTCACTCACTCACTTAATGCACTCACTCACTCACTCACTCACTCACTCACTCACT	1767
QY	481	GlnSerProGlnHisAlaGluMetCYsAluMetIleThrAlaGlyProThrPheAlaGluGlu	500
Db	1768	CAGTCCCCACAGCATGACAGAGATGTGCTCCACACCGCTGGCCCGCCAGTTCGCTGAAGAG	1827
QY	501	MetGlyGluThrGlnSerGluTYrSerLeuAspSerSerCYsGluIleuAnGlyAlaPhePheCYs	520
Db	1828	ATGGGAGAGACCCACAGTCTGAAGTACTCAAGATTCTAAGCTGTGAAGACGGAGGCGCTTCTTCTGC	1887
QY	521	AsnGluCYsAspArgPheArgPheSerGlyGlnAlaSerLeuLYsArgHisIleuLeuGlnThr	540
Db	1888	AATGAGTGTGACTGCGCTTCTCTGAGAGAGCGCTCACTCAAGAGGCAACAGCTGTCAACAC	1947
QY	541	HisSerAspLYsProTYrLYsCYsAspArgCYsGlnAlaSerPheArgTYrLYsGlyAsn	560
Db	1948	CACAGTGCACAAACCTTAAGTGTGACCGCTGCAGGCGCTCTCCGCTCAAGAGGGCAAC	2007
QY	561	LeuAlaSerHisLYsIleThrValHisIleThrGlyGluLYsProTYrArgCYsAsnIleCYsGly	580
Db	2008	CTCGCGACACCAAGACCGCTCATACCGGTGAGAAACCTTAATGCTTGCATCATCTGTGGG	2067
QY	581	AlaGlnPheAsnArgProAlaAsnLeuLYsThrHisIleThrArgIleHisSerGlyGluLYs	600
Db	2068	GCCCGAGTTCACCGGCGCAGCCACCTGAAAACCACTGCAATTCACCTCGAGAGAGAG	2127
QY	601	ProTYrLYsCYsGluThrCYsGlyAlaArgPheValGlnValAlaHisLYsLeuArgAlaHis	620
Db	2128	CCCTTAACAAATCGAAACCTGGCGAGCGCAGATTGTGAACGATGGGCCACTCGTGGCCAT	2187
QY	621	ValIleuIleHisIleThrGlyGluLYsArgProTYrProCYsGlyIleCYsGlyThrArgPheArg	640
Db	2188	GGGCTTATTCACACTGTGTGAGAAAGCCCTATCCCTGTGAATCTGTGGACCCGGTTCGGG	2247
QY	641	HisLeuGlnIleThrLeuLYsSerHisLYsLeuArgIleHisIleThrGlyGluLYsArgProTYrHisCYs	660
Db	2248	CACCTTCAGACTGTGAAGAGCACCCTGGAAATCCACACAGAGAGAAACCTTACCATTTGT	2307
QY	661	GluLYsCYsAsnLeuHisPheArgHisLYsSerGlnLeuArgLeuHisLYsLeuArgGluLYs	680
Db	2308	GAGAAAGTGAACCTGCAATTTCCGTCACAAAGCCAGCGCGCACTTCACTTGGCGCAAGAG	2367
QY	681	HisGlyAlaIleIleThrAsnThrLYsValGlnTYrArgValSerAlaIleAspLeuProPro	700
Db	2368	CATGGCGCCATCAACCAACCAAGGTGCAATACCGCGTGTGACGCACTGAAGCTGCTCGG	2427
QY	701	GluLeuProLYsAlaCYs 706	
Db	2428	GAGCTCCCAAGACCTGC 2445	

XX 21-OCT-2004 (first entry)  
 XX Human NF-kappaB pathway-associated gene SeqID65.  
 XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;  
 XX antirheumatic; antirheumatic; gastrointestinal-Gen; antiaesthetic;  
 XX antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;  
 XX immunosuppressive; vulnery; gene therapy; immune disorder;  
 XX inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;  
 XX hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;  
 XX hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;  
 XX X-linked andidrotic ectodermal dysplasia; immunodeficiency;  
 XX viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;  
 XX viral replication; host cell survival; evasion of immune response;  
 XX rheumatoid arthritis; inflammatory bowel disease; colitis; ascites;  
 XX atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;  
 XX autoimmune disorder; hyper immune activity;  
 XX aberrant acute phase response; hypercongenital condition; birth defect;  
 XX necrotic lesion; wound; organ transplant rejection;  
 XX aberrant signal transduction; proliferating disorder; cancer;  
 XX HIV propagation; gene; ds; human.  
 XX Homo sapiens.  
 XX MO2004065577-A2.  
 XX 05-AUG-2004.  
 XX 13-JAN-2004; 2004MO-US000798.  
 XX 14-JAN-2003; 2003JUS-0440068P.  
 XX 12-MAY-2003; 2003JUS-0469757P.  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX Nadler SG, Neubauer MG, Feder JN, Carman J;  
 XX WPI, 2004-562168/54.  
 XX P-PSDB; ADRI4065.  
 XX New isolated polynucleotides and polypeptides associated with NF-kappaB  
 XX pathway, useful for diagnosing, treating, or preventing disorders or  
 XX diseases associated with NF-kappaB pathway.  
 XX Claim 1; SEQ ID NO 65; 237bp; English.  
 XX This invention relates to the novel association of protein sequences (and  
 XX the genes which encode them) to the NF-kappaB pathway. The invention may  
 XX be useful for the production of compounds with an antiinflammatory,  
 XX cyostatic, hepatotropic, virucide, antirheumatic, antiaesthetic,  
 XX gastrointestinal-Gen, antiaesthetic, antiarteriosclerotic,  
 XX immunomodulator, cerebroprotective, vasotropic, immunosuppressive or  
 XX vulnery activity or for gene therapy. The proteins and nucleotides are  
 XX useful for diagnosing, preventing, treating, or ameliorating conditions  
 XX or diseases associated with the NF-kappaB pathway. The condition is an  
 XX immune disorder, an inflammatory disorder, an inflammatory disorder  
 XX related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,  
 XX hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM  
 XX syndromes, hypohidrotic ectodermal dysplasia, X-linked andidrotic  
 XX ectodermal dysplasia, immunodeficiency viral infections, HIV-1, HTLV-1,  
 XX hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell  
 XX survival, evasion of immune responses, rheumatoid arthritis, inflammatory  
 XX bowel disease, colitis, ascites, atherosclerosis, cachexia, euthyroid sick  
 XX syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper  
 XX immune activity, disorders related to aberrant acute phase responses,  
 XX hypercongenital conditions, birth defects, necrotic lesions, wounds,  
 XX organ transplant rejection, conditions related to organ transplant  
 XX rejection, disorders related to aberrant signal transduction,  
 XX proliferating disorders, cancers and HIV propagation in cells infected  
 XX with other viruses. The present sequence is that of a human gene which is  
 XX subject to the novel association with the NF-kappaB pathway of the  
 XX invention. Note: This sequence does not appear in the specification but

CC was obtained by the indexer from Genbank.  
 XX SQ Sequence 3536 BP; 936 A; 943 C; 835 G; 822 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1,4e-192 Length: 3536  
 Score: 3793.00 Matches: 706  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 13 Gaps: 0  
 US-10-755-889-18 (1-706) x ADRI4064 (1-3536)  
 QY 1 MetAlaSerProAlaAspSerCysIleGlnPheThrArgHisAlaSerAspValLeuLeu 20  
 DB 328 ATGGCTGCGCCGCGACGAGCTGATCCAGTTCCACCCGCGCATCGAGATGTTCTTCTC 387  
 QY 21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValIleValIleSerArg 40  
 DB 388 AACCTTAATCGTCTCGGAGTGAAGACATCTTGACTGATGTTGATGAGCGGT 447  
 QY 41 GluGlnPheArgAlaHisLeuThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle 60  
 DB 448 GAGCAGTTATGAGCCCATTAACCGGTCCCATGCGCTGCGAGTGGCTGTTCTATGACATC 507  
 QY 61 PheThrAspGlnLeuLeuPheCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80  
 DB 508 TTTCACAGACCAAGTTGAATGCAACCTTGATGATCATCTGATCTTGATGATCAACCTT 567  
 QY 81 GluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100  
 DB 568 GAGGATTTGTCATCCTCTGAGCTTCATGATCATCATCTCGGCTCAATTTGCGGAGGGCC 627  
 QY 101 AsnIleMetAlaValMetAlaThrAlaMetCylTyrLeuGlnMetGluHisValIleAspThr 120  
 DB 628 AACATCATGCTGTGATGAGCCGACGCTATGATCTGACATATGACATATTTGTGACACT 687  
 QY 121 CysArgGlyPheIleValIleSerGluIleGluMetValIleSerAlaIleValSerProArg 140  
 DB 688 TGCCGAAAGTTATTAAGCCAGTGAAGCAAGATGTTTCTGCCATCAAGCTCTCTGCT 747  
 QY 141 GluGluPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160  
 DB 748 GAAAGTCTCTCAACAGCCGAGTGTGATGCCCAAGACATCATGCGGATCGGCTGCT 807  
 QY 161 GluValIleValIleAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe 180  
 DB 808 GAGGTGTGAGAAACAACCTGACACTGAGAGCGCCCTGGGTGTGAGAGCAGAGCTTT 867  
 QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200  
 DB 868 GCCCCGAGCTGTACAGTGGCTGTGCACACCGCCAGCTCTTATTCATGATACAGCCAC 927  
 QY 201 LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspValIleArgMetProVal 220  
 DB 928 CTCCCTGTAGCAGAGCTCTCTCTTCCGATGAGAGTTCCGGGATGCGGATGCTGTG 987  
 QY 221 AlaAsnProPheProIleGluArgAlaLeuProCysAspSerAlaArgProValProGly 240  
 DB 988 GCCAACCCCTTCCCAAGAGCGGGACATCCCATGTGATGATGCCAGGCGAGTCCCTGTG 1047  
 QY 241 GluTyrSerArgProThrLeuGluValIleSerProAsnValCysHisSerAsnIleTyrSer 260  
 DB 1048 GAGTACAGCGCGGCGACTTTGAGAGTGTCCCAAGTGTGTCCACAGCAATATCTATTTCA 1107  
 QY 261 ProIleGluThrIleProGluGluAlaArgSerAspMetHisTyrSerValIleGluGly 280  
 DB 1108 CCCAAGAAACAATCCCAAGAGGCAAGAGCAAGATGATGACATCATGATGCTGTGAGGG 1167  
 QY 281 LeuIleProAlaIleProSerAlaArgAsnAlaProTyrPheProCysAspIleValIleSer 300  
 DB 1168 CTAAACCTGTGCTGCTCCCTCAGCCGAAATGCCCCCTACTTCCCTGTGACAAAGGCCAGC 1227

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QY 301 LysGluGluGluGluArgProSerSerGluAspGluIleAlaLeuHisIspheGluProProAsn 320
DB 1228 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1287
QY 321 AlaProLeuAsnArgGlyGlyLeuValSerProGlnSerProGlnSerProGlnSerProGln 340
DB 1288 GCACCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1347
QY 341 ProAsnSerProThrGluAlaCysSerSerIysAsnAlaCysIleLeuGlnAlaSerGly 360
DB 1348 CCCACTGCGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1407
QY 361 SerProProAlaIysSerProThrAspProIysAlaCysAsnIleIleValSerGlyPhe 380
DB 1408 TCCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1467
QY 381 IleValLeuAsnSerIleAsnAlaAlaSerProGlyGlyProGluGlnAlaGluLeu 400
DB 1468 ATCTGTCTCAACAGCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1527
QY 401 GlyArgLeuSerProAlaIleThrAlaProProAlaCysGlnProMetGluPro 420
DB 1528 GGGCCCTTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1587
QY 421 GluAsnLeuAspLeuGlnSerProThrIleLeuSerAlaSerGlyGlyAspSerThrIle 440
DB 1588 GAGAACTTGACCTCCAGTCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1647
QY 441 ProGlnAlaSerAlaGluAsnAlaIleValAsnArgSerMetThrGlySerProArgSer 460
DB 1648 CCACAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1707
QY 461 SerSerGluSerHisSerProLeuThrMetHisProProIysCysThrSerCysGlySer 480
DB 1708 AGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1767
QY 481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500
DB 1768 CAGTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1827
QY 501 MetGlyGluThrGlnSerGlyIleSerAspSerSerCysGluAsnGlyAlaPhePheCys 520
DB 1828 ATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1887
QY 521 AsnGlyCysAspCysArgPheSerGluGluAlaSerLeuIleArgHisIleThrLeuGlnThr 540
DB 1888 AATAGGTGTGAGTGGCTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1947
QY 541 HisSerAspIysProIleCysAspArgCysGlnAlaSerPheArgIleGlyValAsn 560
DB 1948 CACAGTGAACAACCTTCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2007
QY 561 LeuAlaSerHisIleThrValHisIleThrGlyGlyProIleArgCysAsnIleCysGly 580
DB 2008 CTCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2067
QY 581 AlaGlnPheAsnArgProAlaAsnLeuIleThrHisIleThrArgIleHisSerGlyGluIys 600
DB 2068 GCCCAGTTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2127
QY 601 ProIleIysCysGluThrCysGlyAlaArgPheValGlnValAlaHisIleLeuArgAlaHis 620
DB 2128 CCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2187
QY 621 ValIleuIleHisIleThrGlyGlyLeuProIleProCysGlnIleCysGlyThrArgPheArg 640
DB 2188 GTGCTTATTCACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2247
QY 641 HisIleuGlnThrLeuIleSerHisIleLeuArgIleHisIleThrGlyGlyLeuProIleHisCys 660
DB 2248 CACCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2307

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QY 661 GluIysCysAsnLeuHisIspheArgHisIleSerSerGluLeuAspLeuHisIleuArgGlnIys 680
DB 2308 GAGAGAGTGAACCTTCCATTTTCCCTCAACAAAGCAGCTGAGATTCACTTGGCCCAAG 2367
QY 681 HisGlyAlaIleThrAsnThrIleValGlnIleArgValSerAlaThrAspLeuProPro 700
DB 2368 CATGGCGCCATTCACCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2427
QY 701 GluLeuProIysAlaCys 706
DB 2428 GAGCTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2445

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RESULT 6  
ADY19589 standard, DNA; 3536 BP.  
ID ADY19589 standard, DNA; 3536 BP.  
AC ADY19589;  
XX  
XX  
DT 05-MAY-2005 (first entry)  
XX  
XX  
DE DNA encoding a PRO polypeptide, SEQ ID NO 5395.  
XX  
XX  
KW Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
KW Antineumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;  
KW Antichyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;  
KW Virucide; Gastrointestinal-Gen.; Antiparasitic; Antiaesthetic;  
KW Antiallergic; ds; gene; diagnosis.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN W02005016962-A2.  
XX  
XX  
PD 24-FEB-2005.  
XX  
XX  
PF 11-AUG-2004; 2004MO-US026249.  
XX  
XX  
PR 11-AUG-2003; 2003US-0493546P.  
XX  
XX  
PA (GERTH ) GENENTECH INC.  
XX  
XX  
PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;  
XX  
XX  
DR WPI; 2005-182330/19.  
XX  
XX  
PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and  
PT treating an immune related disorder, e.g. systemic lupus erythematosus,  
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.  
XX  
XX  
PS Claim 1; SEQ ID NO 5395; 1589bp; English.  
XX  
XX  
CC The invention relates to an isolated nucleic acid encoding a PRO  
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,  
CC composition, and method are useful for diagnosing and treating an immune  
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid  
CC arthritis. The present sequence represents a PRO polypeptide.  
XX  
XX  
SQ Sequence 3536 BP; 936 A; 943 C; 835 G; 822 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1,4e-192 Length: 3536  
Score: 3793.00 Matches: 706  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 14 Gaps: 0

US-10-755-889-18 (1-706) x ADY19589 (1-3536)

```

QY 1 MetAlaSerProAlaAspSerCysIleGlnPheThrArgHisAlaSerAspValLeuLeu 20
DB 328 ATGGCCTCGCGGCTGACAGCTGTATCCAGTTCAACCGGCATGCGAGATGTTCTTC 387
QY 21 AsnLeuAsnArgLeuAspSerArgAspIleLeuThrAspValIleValIleValSerArg 40

```

Db 388 AACCTTAATCGTCCGAGTGGAGACATCTTGAAGATGTTGTCTATTGTGTGAGCCCT 447  
Qy 41 GUGlnPheArgAlaHisIstYrThrValLeuMetAlaCysSerGlyLeuPheYrSerIle 60  
Db 448 GAGCACTTTAGAGCCCATAAACGCTTCATGCTGAGCTGCGCTGTTCTATACATC 507  
Qy 61 PheThrAspGlnLeuIstYrCysAsnLeuSerValIleAsnLeuAspProGlnIleAsnPro 80  
Db 508 TTACAGACCAAGTTGAATGCAACCTTAGTGATGATCAATCTAGATCCTGAGATCAACCT 567  
Qy 81 GUGlyPheCysIleLeuLeuAspPheMetYrThrSerArgLeuAsnLeuArgGlyIst 100  
Db 568 GAGGATTTCTGATCTCTCGATCTTCAATGATCAATCTCGCTCAATTTGGGAGAGGC 627  
Qy 101 AsnIleMetAlaValMetAlaThrAlaMetYrLeuGlnMetGlnHisValValAspThr 120  
Db 628 AACATATGCTGTGATGCGCACGCGCTATGTACTCTCAGATGAGCATGTTGTGACACT 687  
Qy 121 CysArgIstPheIleIstYrAlaSerGlnIstGlnMetValSerAlaIleIstYrProArg 140  
Db 688 TGCAGGAAGTTTATTAAGCCAGATGAAAGCAGAGATGTTTCTGCATCAAGCTCTCGT 747  
Qy 141 GUGlnPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaIstYrArgGlyArg 160  
Db 748 GAAAGATTCTCTCAACAGCGGAGTGTGATGCGCCCAAGACATCATGCGCTATCGGGTCCG 807  
Qy 161 GluValValGlnIstAsnLeuPheLeuArgSerAlaProGlyCysGlnSerArgAlaPhe 180  
Db 808 GAGGTGTGTGAAGAACACCTGCACATGAGAGCGCCCTGGGTGTGAGACAAAGCTT 867  
Qy 181 AlaProSerLeuIstYrSerGlyLeuSerThrProAlaSerIstYrSerMetYrSerHis 200  
Db 868 GCCCCAGCTGTACAGTGGCTGTGTCCACCGCCAGCTCTTATTCATGTCACAGCAC 927  
Qy 201 LeuProValSerSerLeuLeuPheSerAspGlnIstPheArgAspValArgMetProVal 220  
Db 928 CTCCTGTGACGACCTCTCTCTCCGATGAGAGATTTGGGATGTCCGAGTGCCTGCG 987  
Qy 221 AlaAsnProPheProIstYrGlnIstArgAlaLeuProCysAspSerAlaArgProValProGly 240  
Db 988 GCCAAGCCCTTCCCAAGAGCGCGCTCTCCATGTGATGTGCCAGGCCAGTCCCTGGT 1047  
Qy 241 GlnTyrSerArgProIstYrLeuGlnIstYrProAsnValCysHisSerAsnIleYrSer 260  
Db 1048 GAGTACAGCGCGGACGATTTGAGAGTGTCCCAAGTGTGTGCACAGCAATATCTATCA 1107  
Qy 261 ProIstYrGlnIstYrProGlnIstYrArgSerAspMetHisIstYrSerValAlaGlyIst 280  
Db 1108 CCCAAGGAACATCCCAAGAGGACAGAGTGTATGTCACTACAGTGTGCTGAGGGC 1167  
Qy 281 LeuIstYrProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspValAsp 300  
Db 1168 CTCAAACTCTGCTGCTCCCTCAGCGCCGAATGCCCCCTCACTTCCCTGTGTGCAAGCGCACG 1227  
Qy 301 IstYrGlnIstYrArgProSerSerGlnAspGlnIleIstYrHisPheGlnIstYrProAsn 320  
Db 1228 AAGAGAAAGAGAGACCTCTCTCGAAGATGAGATGCTCTGCAATTCGAGCCCCCAAT 1287  
Qy 321 AlaProLeuAsnArgIstYrGlyLeuValSerProGlnSerProGlnIstYrSerAspCysGln 340  
Db 1288 GCACCTCTGAACCGGAAGGCTGTGTATGTTCACAGAGCCGCCAGAAATGTGCTGCGAG 1347  
Qy 341 ProAsnSerProThrGlnIstYrCysSerSerIstYrAsnAlaCysIleIstYrGlnIstYr 360  
Db 1348 CCCAACTCGCCCAAGAGGCTGTGACAGATGATCTCTGCAATCTCCAGGCTTCTGCGC 1407  
Qy 361 SerProProAlaIstYrSerProThrAspProIstYrAlaCysAsnIstYrIstYrIstYrPhe 380  
Db 1408 TCCCTTCAGCAAGAGCCCACTGACCCCAAGAGCTGTGCAATGTGAAGAAATCAAGATTC 1467  
Qy 381 IleValLeuAsnSerLeuAsnGlnAsnAlaIstYrProGlyIstYrProGlnIstYrAlaGlyLeu 400

Db 1468 ATGCTGTCAACAGCCTCAACCAAGATGCAACCAAGGAGGCGCTGAGAGGCTGAGCTG 1527  
Qy 401 GlyArgLeuSerProArgAlaIstYrThrAlaProProAlaCysGlnProMetGlnPro 420  
Db 1528 GGCCTGCTTTTCCCAAGAGCTTACAGCGGCCCACTGCTGTGCACACCCATGAGGCT 1587  
Qy 421 GluAsnLeuAspLeuGlnIstYrProThrIstYrIstYrIstYrIstYrIstYrIstYrIstYr 440  
Db 1588 GAGAACTTGAACCTCAAGTCCCAACCAAGCTGAGATGCGACAGGAGGAGGACTCCACATC 1647  
Qy 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460  
Db 1648 CCACAAAGCCAGCGGCTCAATACATCTGTAAACAGTCTCATACAGGCTCTCCCGCACG 1707  
Qy 461 SerSerGlnIstYrSerProLeuIstYrMetHisProProIstYrCysThrSerCysGlySer 480  
Db 1708 AGCAGAGAGGCACTCAACCACTTACATGACACCCCGAAGTGCACGTCCTGCGGCTCT 1767  
Qy 481 GlnSerProGlnHisAlaGlnMetCysLeuHisIstYrAlaGlyProThrPheAlaGlnIst 500  
Db 1768 CAGTCCCAACAGCATGAGAGATGTGCTCCACACCGCTGCGCCACGTTGCTGAGAG 1827  
Qy 501 MetGlyGlnIstYrGlnIstYrSerArgSerSerCysGlnAsnGlyAlaPhePheCys 520  
Db 1828 ATGGGAGAGACCCAGCTGATGATCTCAGATTTCTAGCTGTGAGAAAGCGGCTTCTTCTGC 1887  
Qy 521 AsnGlnCysAspCysArgPheSerGlnIstYrIstYrIstYrIstYrIstYrIstYrIstYr 540  
Db 1888 AATGATGTGACTGCGGCTTCTGTGAGAGGCTCTCAAGAGGACACGCTGACAGACC 1947  
Qy 541 HisSerAspIstYrProTyrIstYrCysAspArgCysGlnAlaSerPheArgTyrIstYrIstYr 560  
Db 1948 CACAGTGAACAACTCAACAGTGTACCGCTCCAGGCTCTCTCCGCTACAAAGGCAAC 2007  
Qy 561 LeuAlaSerHisIstYrThrValHisIstYrGlyIstYrProTyrArgCysAsnIleCysGly 580  
Db 2008 CTCGCGACGCAACAGCCCTTCATACCGGTGAGAAACCTTATCGTTGCAACATCTGTGG 2067  
Qy 581 AlaGlnPheAsnArgProAlaAsnLeuIstYrHisIstYrIstYrIstYrIstYrIstYrIstYr 600  
Db 2068 GCCAGTTAAACCGGCAACCACTGAAACCCACACTGAAATCACTGTGAGAGAG 2127  
Qy 601 ProTyrIstYrCysGlnIstYrCysGlyAlaArgPheValGlnValAlaHisIstYrArgAlaHis 620  
Db 2128 CCTCAAAATGCGAAACCTGCGAGCGAGATTTGTACAGTGTGCCACTCCGTGCCAT 2187  
Qy 621 ValLeuIleHisIstYrGlyIstYrProTyrProCysGlnIstYrIstYrIstYrIstYrIstYr 640  
Db 2188 GTGCTTATCAACATGTGTGAGAGGCTCTCTCTGTGAATCTGTGGCACCGGTTTCCCG 2247  
Qy 641 HisIstYrGlnIstYrLeuIstYrSerHisIstYrArgIleHisIstYrGlyIstYrProTyrHisCys 660  
Db 2248 CACCTTCAACCTTGAAGGCCCTGCGAATTCACACAGAGAGAAACCTTACCTTGT 2307  
Qy 661 GlnIstYrCysAsnLeuHisPheArgHisIstYrSerGlnLeuArgLeuHisIstYrArgGlnIstYr 680  
Db 2308 GAGAAATGTACCTGATTTCTGTCACAAAGCAGCTGCACTTGTGGCGCAGAG 2367  
Qy 681 HisGlyAlaIleThrAsnThrIstYrValGlnTyrArgValSerAlaThrAspLeuProPro 700  
Db 2368 CATGGCGCATACCAACCAAGGTGCAATCCGCTGTGAGCCACTGACCTGCTCCG 2427  
Qy 701 GlnLeuProIstYrAlaCys 706  
Db 2428 GAGCTCCCAAGAGCTGC 2445  
RESULT 7  
ADL82846  
ID ADL82846 standard; cDNA; 3537 BP.  
XX  
AC ADL82846;  
XX  
DT 17-JUN-2004 (first entry)





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Db      1588 GAGAACTTGACCTCCAGTCCCAACCAAGCTGAGTGCACGGGGAGGAGACTCCACATC 1647
Qy      441 ProGlnAlaSerArgLeuAsnAnll eValAsnArgSerMetThrGlySerProArgSer 460
Db      1648 CCACAAGCCAGCGCGCTCATATACATCGTTAACAGGTCCATGACGGGCTCTCCGCCACAG 1707
Qy      461 SerSerGlySerHisSerProLeuTyMetHisProProLysSerThrSerGlySer 480
Db      1708 AGCAGGAGAGCCACTCCACTCTTCAATGACACCCCCCAAGTGCACGTCTCGGCTCTT 1767
Qy      481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500
Db      1768 CAGTCCCAACAGATGAGATGCTGCTCCACACGGCTGGCCCCAGTTCCCTCGAGAG 1827
Qy      501 MetGlyGluThrGlnSerGluTySerSerPheSerSerCysGluAsnGlyAlaPhePheCys 520
Db      1828 ATGGGAGAGACCCAGCTGAGTACTCAGATTCTTACGCTGTGAGAACCGGGCTTCTTCTGC 1887
Qy      521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540
Db      1888 AATGAGTGTACTGCGCTTCTCTGAGAGAGGCTCTCAAGAGGACACAGCTGCAAGCC 1947
Qy      541 HisSerAspLysProTyTrpLysCysAspArgCysGlnAlaSerPheArgTyTrpGlyAsn 560
Db      1948 CACAGTGAACAACCTTACAGAGTGAACCGCTGCAGGGCTCTTCCGCTTACAGAGGCAAC 2007
Qy      561 LeuAlaSerHisLysThrValHisThrGlyGluLysProTyArgCysAsnLysCysGly 580
Db      2008 CTCGCAGACCAAGACCGTCCATACCGGTGAGAAACCTTATCGTTGCAACATCTGTGG 2067
Qy      581 AlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgLysHisSerGlyGluLys 600
Db      2068 GCCCAGTTCAACCGGCGACCAACCTGAAACCACTGAATTCATCTGAGAGAGAG 2127
Qy      601 ProTyTrpLysCysGluThrCysGlyAlaArgPheValGlnValAlaHisLeuArgAlaHis 620
Db      2128 CCTTACAAATGCCAAACCTCGAGACCAAGTTGTACAGGTGGCCACCTCCGTGCCAT 2187
Qy      621 ValLeuLysHisThrGlyGluLysProTyProCysGluLysCysGlyThrArgPheArg 640
Db      2188 GTCTTATCCACACTGGTGTGAGAAACCTTATCCCTGTGAAATCTGTGGCACCCGTTCCG 2247
Qy      641 HisLeuGlnThrLeuLysSerHisLeuArgLysHisThrGlyGluLysProTyTrpLysCys 660
Db      2248 CACCTTCAAGCTGTGAAGACCACTGCGAATCCACACAGAGAGAAACCTTACCATGT 2307
Qy      661 GluLysCysAsnLeuHisPheArgHisLysSerGlnLeuArgLeuHisLeuArgGluLys 680
Db      2308 GAAAGGTGAACCTGCACTTCCGTCAAAAGCCAGCTGCACTTCACTTGGCCAGAGAG 2367
Qy      681 HisGlyAlaLeuThrAsnThrLysValGlnTyArgValSerAlaThrAspLeuProPro 700
Db      2368 CATGGCGCATCAACCAACCAAGGTGATACCGCGTGCAGCACTGACTGCGCTCCG 2427
Qy      701 GluLeuProLysAlaCys 706
Db      2428 GAGCTCCCAAGCGTGC 2445

```

RESULT 8  
ADY15005  
ID ADY15005 standard; DNA, 3630 BP.  
XX  
AC ADY15005;  
DT 05-MAY-2005 (first entry)  
XX  
DE DNA encoding a PRO polypeptide, SEQ ID NO 811.  
XX  
KW Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
KW Antineumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;  
KW Antihypoid; Antidiabetic; Nephrotoxic; CNS-gen.; Hepatocytotoxic;  
KW Virucide; Gastrointestinal-Gen.; Antiporiatic; Antiaesthetic;

```

KW Antiallergic; ds; gene; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2005016962-A2.
XX
PD 24-FEB-2005.
XX
PF 11-AUG-2004; 2004WO-US026249.
XX
PR 11-AUG-2003; 2003US-0493546P.
XX
PA (GENTH) GENENTECH INC.
XX
PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX
DR WPI; 2005-182330/19.
XX
PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
PS Claim 1; SEQ ID NO 811, 158pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a DNA encoding a PRO
XX polypeptide.
XX
SQ Sequence 3630 BP; 955 A; 959 C; 839 G; 877 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1,02e-191 Length: 3630
Score: 3777.00 Matches: 703
Percent Similarity: 99.7% Conserved: 1
Best Local Similarity: 99.6% Mismatches: 2
Query Match: 99.6% Indels: 0
DB: 14 Gaps: 0
US-10-755-889-18 (1-706) x ADY15005 (1-3630)
Qy      1 MetAlaSerProAlaAspSerCysIleGlnPheThrArgHisAlaSerAspValLeuLeu 20
Db      421 ATGGCTTCCCGGCTGACAGCTGTATCCAGTTCAACCCGCAAGCCAGTATGTTCTTCTC 480
Qy      21 AsnLeuAsnArgLeuLysSerArgAspLysLeuThrAspValAlaValAlaSerArg 40
Db      481 AACCTTAACTCGTCTCCGAGTGCAGACATCTGACTGATGTTGTGTCATGTTGAGACCGT 540
Qy      41 GluGlnPheArgAlaHisLysThrValLeuMetAlaCysSerGlyLeuPheTySerIle 60
Db      541 GAGCATTTTAAAGCCCATTAACCGCTTCATAGGCTCGAGGCTGTGCTTCTTATACATC 600
Qy      61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
Db      601 TTTCAGACCAAGTGAATGCAACCTTATGATGATTAATCTAGATCTTAAGATCAACCT 660
Qy      81 GluGlyPheCysIleLeuLeuAspPheMetTyTrpHisArgLeuAsnLeuArgGluGly 100
Db      661 GAGGATTTCTGATCTCTCGATCTTCATGTACATCTCGGCTCAATTTGGCGAGAGGG 720
Qy      101 AsnIleMetAlaValMetAlaThrAlaMetTyTrpGlnMetGlnHisValAlaAspThr 120
Db      721 AACATCATGCTGTGTGATGCGCAACGGCTATGTACTTCGCAATGAGCATGTTGTGACACT 780
Qy      121 CysArgLysPheLysLeuLysAlaSerGluAlaGluMetValSerAlaLysProProArg 140
Db      781 TGCCGGAAGTTTATTAAGCAGGTGAGAGAGAGATGTTTCTGCCATCAAGCTCTCTGT 840
Qy      141 GluGlnPheLeuAsnSerArgMetLeuMetProGlnAspLysMetAlaTyArgGlyArg 160

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Db 841 GAAAGATTCTCAACAGCCGGATGCTGATGCCCAAGATCATGCGCTTACGGGGCTCT 900  
 Qy 161 GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe 180  
 Db 901 GAGGTGGTGAAGAACCACTGACCTGAGAGAGCGCCCTGGTGTGAGACAGAGCCTTT 960  
 Qy 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200  
 Db 961 GCCCCAGCCTGTACAGTGGCTGTCCACACCGCACCTCTTAATTCACAGTACAGCAC 1020  
 Qy 201 LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspValArgMetProVal 220  
 Db 1021 CTCCCTGTGACAGACCTCTCTCTCTCCGATGAGAGAGTTTGGAGTTCGGAGTCCCTG 1080  
 Qy 221 AlaAsnProPheProLeuGluArgAlaLeuProCysAspSerAlaArgProValProGly 240  
 Db 1081 GCCAACCCCTTCCCAAGAGAGCGGACCTCCCATGTATGTCACAGCCAGTCCCTGCT 1140  
 Qy 241 GluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyrSer 260  
 Db 1141 GAGTACAGCCGGCCGACTTGGAGTGTCCCAATGTGTGCCACACCAATATCTATTCA 1200  
 Qy 261 ProGluGluThrIleProGluGluAlaArgSerAspMetHisTyrSerValAlaGluGly 280  
 Db 1201 CCCAAGGAAACAAATCCAGAGAGGACAGAGATGATGCACTACAGTGTGGCTGAGGGC 1260  
 Qy 281 LeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLysAlaSer 300  
 Db 1261 CTCAACCTGCTGCCCCCTCAGCCCGAAATGCCCCCTACTTCCCTTGTGACAGAGCCAGC 1320  
 Qy 301 LysGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAsn 320  
 Db 1321 AAGAAGAAAGAGAGACCTCTCGAGAGATGAGATCCCTGCACTTTCGAGCCCCCAAT 1380  
 Qy 321 AlaProLeuAsnArgGlySerGlyLeuValSerProGluSerProGluLysSerAspCysGln 340  
 Db 1381 GCACCCCTGAAACCGAAGGGGTGTGTTAGTTCACAGAGAGCCCAAGAAATCTGACTGACG 1440  
 Qy 341 ProAsnSerProThrGluAlaCysSerSerLysAsnAlaCysIleLeuGluAlaSerGly 360  
 Db 1441 CCCAATCTGCCCCAGAGTCTCTGACAGCATGTAAGATGCTCTGACAGGCTTCTGGC 1500  
 Qy 361 SerProProAlaLysSerProThrAspProLysAlaCysAsnIlePheLysTyrLysPhe 380  
 Db 1501 TCCCTCTCAGCAGAGAGCCCACTGACCCCAACCTGCAACTGGAAGAAATACAAATTC 1560  
 Qy 381 IleValLeuAsnSerLeuAsnGlnAsnAlaLysProGlyGlyProGluGlnAlaGluLeu 400  
 Db 1561 ATCTGTCTCAACAGCTTCAACAGAAATGCCAAACAGAGGGGCTGAGAGGCTGAGCTG 1620  
 Qy 401 GluLysLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProProMetGluPro 420  
 Db 1621 GGGCCGCTTTCCCAAGAGCTTACAGGCCCCCACTGCTGCTGACAGCCCATGAGAGCT 1680  
 Qy 421 GluAsnLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIle 440  
 Db 1681 GAGAACTTGAACCTCCAGTCCCAACCAAGCTGAGTGCACGGGAGAGAGATCCACACATC 1740  
 Qy 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460  
 Db 1741 CCACAGAGCAGCCGGCTCAATACATCGTTAAAGGTTCACAGAGGGGCTCTCCCGCAGC 1800  
 Qy 461 SerSerGluSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480  
 Db 1801 AGCAGCGAGAGCCACTACCACTTACATGCACCCCCGAAGTGCACCTCTGGGGCTCT 1860  
 Qy 481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500  
 Db 1861 CAGTCCCAAGCATGAGAGATGAGTCTCCACACCGCTGAGCCCACTTCCCTGAGGAG 1920  
 Qy 501 MetGlyGluThrGlnSerGluTyrSerArgSerSerCysGluAsnGlyAlaPhePheCys 520  
 Db 1921 ATGGAGAGACCAAGTGTGATCTCAGATTCTAGCTGTGAGAAAGGGGGCTTCTTCTGCT 1980

Qy 521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540  
 Db 1981 AATGAGTGTGACTGCGGCTTCTCTGAGAGGCTTCTCAAGAGGACACAGCTGACAGAC 2040  
 Qy 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560  
 Db 2041 CACGTGACAAACCTTACAAAGTGTGACCGCTGACAGGCTCTCCGCTTACAGAGGAC 2100  
 Qy 561 LeuAlaSerHisLysThrValHisThrGlyGluLysProTyrArgCysAsnIleCysGly 580  
 Db 2101 CTGCGACGACACAGAGCCCTTCCATACCGGTGAGAAACCTTATGTGCAACATCTGGG 2160  
 Qy 581 AlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgIleHisSerGlyGluLys 600  
 Db 2161 GCCCAGTTCACACCGGCGACGAACTGAAACCCACACTGAAATTCACCTTGAGAGAG 2220  
 Qy 601 ProTyrLysCysGluThrCysGlyAlaArgPheValAlaHisLeuArgAlaHis 620  
 Db 2221 CCTTACAAATGCAAACTGCGAGCCAGATTTGTACAGTGGCCACCTCCGTGCCAT 2280  
 Qy 621 ValLeuIleHisThrGlyGluLysProTyrProCysGluIleCysGlyThrArgPheArg 640  
 Db 2281 GTGCTTATCACAAGTGTGAGAGCCCTATCCCTGGAATCTGTGGCACCCGTTCCGG 2340  
 Qy 641 HisLeuGlnThrLeuLysSerHisLeuArgIleHisThrGlyGluLysProTyrHisCys 660  
 Db 2341 CACCTTCAAGCTCTGAAAGGCCACTGCGAATCCACAGAGAGAAACCTTACCATTTGT 2400  
 Qy 661 GluLysCysAsnLeuHisPheArgHisLysSerGlnLeuArgLeuHisLeuArgGlnLys 680  
 Db 2401 GAGAGGTGACTGCTGATTTCCGTCAACAAAGCCAGCTGCACTTCACTTGGCCAGAG 2460  
 Qy 681 HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700  
 Db 2461 CATGGCGCATTCACCAACACCAAGGTGCAATACCGGTGTCAAGCACTGACCTGCCG 2520  
 Qy 701 GluLeuProLysAlaCys 706  
 Db 2521 GAGCTCCCAAGCCTGC 2538

RESULT 9  
 ADE53822/c  
 ID ADE53822 standard; cDNA; 4506 BP.  
 XX  
 AC ADE53822;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human prostate cancer cDNA #169.  
 XX  
 KW Human; prostate cancer; ss; cDNA combination; differential expression;  
 KW gene.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003190640-A1.  
 XX  
 PD 09-OCT-2003.  
 XX  
 PF 29-MAY-2002; 2002US-00252157.  
 XX  
 PR 31-MAY-2001; 2001US-0295048P.  
 XX  
 PA (FARI/) FARIS M.  
 PA (PEAR/) PEARSON C I.  
 XX  
 PI Faris M, Pearson CI;  
 XX  
 DR WPI; 2003-831619/77.  
 XX  
 PT New combination comprising cDNAs that are differentially expressed in prostate cancer, useful for diagnosing, treating or monitoring the

PT progression of treatment of prostate cancer.  
XX  
PS Claim 1, SEQ ID NO 169; 42pp; English.  
XX  
CC The invention relates to a combination comprising a number of cDNAs  
CC expressed in prostate cancer. The invention also relates to a method for  
CC detecting differential expression of one or more cDNAs in a sample  
CC containing nucleic acids by hybridising a substrate with the nucleic  
CC acids, thus forming one or more hybridisation complexes, detecting  
CC hybridisation complex formation and comparing the complexes formed with  
CC standard complexes, where differences between the standard and the sample  
CC complex formation indicate differential expression of cDNAs in the  
CC sample. The differential expression is diagnostic of prostate cancer. The  
CC invention also relates to proteins and antibodies related to the cDNAs.  
CC The combination is useful for diagnosing, treating or monitoring the  
CC progression of treatment of prostate cancer. The antibodies are useful  
CC for detecting prostate cancer. This sequence represents a human prostate  
CC cancer cDNA of the invention.  
XX  
SO Sequence 4506 BP; 1113 A; 1102 C; 1135 G; 1156 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 1,29e-191 Length: 4506  
Score: 3777.00 Matches: 703  
Percent Similarity: 99.7% Conservative: 1  
Best Local Similarity: 99.6% Mismatches: 2  
Query Match: 99.6% Indels: 0  
DB: 10 Gaps: 0  
  
US-10-755-889-18 (1-706) x ADB53822 (1-4506)  
  
QY 1 MetAlSerProAlaApSerCySileGlnPheThrArgHisAlaSerAapValLeuLeu 20  
DB 3219 ATGACCTCGCGGCTGACAGCTGATTCAGTTCACCGCATGCCAGTATGTTCTTCTC 3160  
  
QY 21 AsnLeuAanArgLeuArgSerArgAspIleLeuThrAspValIleValValSerArg 40  
DB 3159 AACCTTATGCTGTCGCGAGATCGAGACATCTTGACGATGTTGATGTTGGAGCGGT 3100  
  
QY 41 GlnGlnPheArgAlaHisIleValThrValLeuMetAlaCySerGlyLeuPheTyrSerIle 60  
DB 3099 GACACAGTTTGAAGCCCTAAACCGTCTCATGGCCGACGTGGCCCTGTTCTATAGCATC 3040  
  
QY 61 PheThrAspGlnLeuLeuArgCysAanLeuSerValIleAsnLeuAapProGluIleAanPro 80  
DB 3039 TTATACACACCAAGTGAATGACACCTTAGTGATCACTTAGATCCTGAGATCACCTT 2980  
  
QY 81 GlnGlyPheCySileLeuLeuAapPheMetTyrThrSerArgLeuAanLeuArgGlnGly 100  
DB 2979 GAGGAGATTTCGACATCCCTCGGACTTCATGATACACATCTCGGCTCATTTGGCGGAGGCG 2920  
  
QY 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValValAapThr 120  
DB 2919 AACATCATGCTGCTGATGAGCGCACCGCTATGATCACTCGAGATGAGCATGTTGTGACACT 2860  
  
QY 121 CysArgIysPheIleValAlaSerGlnAlaGlnMetValSerAlaIleLeuProProArg 140  
DB 2859 TGCAGGAAGTTTATTAAGCCAGTGAAGACAGATGTTTCTGCAATCAAGCTCTCTGCT 2800  
  
QY 141 GlnGlnPheLeuAanSerArgMetLeuMetProGlnAapIleMetAlaTyrArgGlyArg 160  
DB 2799 GAAGAGTTCTCTCAACACCGGATGCTGATGCCCAACATCANTGGCTATTCGGGGCTGCT 2740  
  
QY 161 GluValValGluAanLeuLeuProLeuArgSerAlaProGlyCySglUserArgAlaPhe 180  
DB 2739 GAGGTGCTGGAACAACCTGCGCACTGAGAGCGCCCTGGGTGTGAGACAGAGCCTTT 2680  
  
QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200  
DB 2679 GCCCCAGACCTGTACAGTGGCTGTCCACACCGCACCTCTTATTCACATGATACGACAC 2620  
  
QY 201 LeuProValSerSerLeuLeuPheSerAapGlnGlnPheArgAapValArgMetProVal 220

DB 2619 CTCCTGTACAGACGCTCTCTTCCGATGAGAGATTTCGGGATGTCGGATGCTGTG 2560  
  
QY 221 AlaAanProPheProValArgAlaLeuProCysAapSerAlaArgProValProGly 240  
DB 2559 GCAACCCCTTCCCAAGAGAGCGGACCTTCCATGTATGATGCGAGGCACTCCCTGCT 2500  
  
QY 241 GlnTyrSerArgProThrLeuGlnValSerProAanValCyHisSerAsnIleTyrSer 260  
DB 2499 GAGTACAGCGGCGCATTTGGAGGTGTCCCAATGTGTGACAGACAAATATCTATTC 2440  
  
QY 261 ProGlyGlnThrIleProGlnGlnAlaArgSerAapMetHisTyrSerValAlaGlnGly 280  
DB 2439 CCCAAGAAACATCCCAAGAAAGCAGAAATGATGACTTACATGATGCTGCTAGAGGC 2380  
  
QY 281 LeuLysProAlaAlaProSerAlaArgAanAlaProTyrPheProCysAapLysAlaSer 300  
DB 2379 CTCGAACCTGCTGCCCCCTCAGCCGGAATGCCCTTACTTCTTGTGACAGGCCAGC 2320  
  
QY 301 LysGlnGlnGluArgProSerSerGlnAapGluIleAlaLeuHisPheGlnProProAan 320  
DB 2319 AAAGAAAGAGAGACCTCTCCGGAAGTGAATTGCTCCATTTGAGGCCCCCAAT 2260  
  
QY 321 AlaProLeuAanArgLysGlyLeuValSerProGlnSerProGlnLysSerAapCyGln 340  
DB 2259 GCACCCCTGAAACCGAAGGCTGTGTTAGTCCACAGAGCCCCAGAAATCTGACTGCGAG 2200  
  
QY 341 ProAanSerProThrGlnAlaCySerSerLysAanAlaCySileuGlnAlaSerGly 360  
DB 2199 CCGACTCGCCACAGAGTCTGACAGATGAAGATGCTGCACTCCAGGCTTCTGGC 2140  
  
QY 361 SerProProAlaLysSerProThrAapProLysAlaCyAanTTPylsTyrLysPhe 380  
DB 2139 TCCCCTCCAGCCAAAGGCCCACTGACCCCAAGCCTGCACTGGAAGAAATACAAATTTC 2080  
  
QY 381 IleValLeuAanSerLeuAanGlnAanAlaLysProGlyGlyProGlnGlnAlaGlnLeu 400  
DB 2079 ATCGTGTCTAAACAGCTCAATGAGATGCAACCAAGAGGCTGAGAGGCTGAGCTG 2020  
  
QY 401 GlyArgLeuSerProArgAlaTyrThrAlaProProAlaCySglInProPrometGluPro 420  
DB 2019 GGGCGCTTTCCTCCAGAGCTTACAGCGCCCACTGCTGCGCACGCCATCGAGCTT 1960  
  
QY 421 GluAanLeuAapLeuGlnSerProThrLysLeuSerAlaSerGlyGluAapSerThrIle 440  
DB 1959 GAGAACCTTGACCTCCAGTCCCAACCAAGCTGAGTGCAGCGGGAGGAGACTCCACATTC 1900  
  
QY 441 ProGlnAlaSerArgLeuAanAsnIleValAanArgSerMetThrGlySerProAanSer 460  
DB 1899 CCACAAAGCCAGCGGCTCAATACATCGTTAACAGGTCCATGACGAGGCTCTCCCGCAC 1840  
  
QY 461 SerSerGlnSerHisSerProLeuTyrMetHisProProLysCyThrSerCySglYser 480  
DB 1839 AGCAGGAGAGCCACTCACCACTTACATGACCCCCCAAGTGCACGTCTCGGCTCT 1780  
  
QY 481 GlnSerProGlnHisAlaGlnMetCySleuHisThrAlaGlyProThrPheAlaGlnGln 500  
DB 1779 CAGTCCCAACAGATCAGAGATGTGCTCCACACCGCTGCGCCCACTTCCCTGAGAGAG 1720  
  
QY 501 MetGlyGlnThrGlnSerGluTyrSerAapSerSerCySglGluAanGlyAlaPhePheCyS 520  
DB 1719 ATGGAGAGAACCCAGCTGATGATCTCAGATTCTAGCTGTGAGAAACGGGGCTTCTCTG 1660  
  
QY 521 AasnGluCyAapCysArgPheSerGlnGluAlaSerLeuLysArgHisThrLeuGlnThr 540  
DB 1659 AATGATGTGACTGCGGCTTCTGTGAGAGGCTTCTCAAGAGGACACAGCTGCGAGACC 1600  
  
QY 541 HisSerAapLysProTyrLysCyAapArgCySglAlaSerPheArgTyrLysGlyAan 560  
DB 1599 CACAGTGAACAACCTTACAAAGTGTACCGCTGCAAGGCTCTTCCGTACAAAGGACAAAC 1540  
  
QY 561 LeuAlaSerHisIleValHisThrGlyGluLysProTyrArgCyAanIleCySglY 580  
DB 1539 CTCGACGACCAAGACCGTCCATCCGGTGAAGAAACCTTATGTGTGCAACATCTGTGG 1480

QY 581 AlAGlnPheAenAaRProAlaAenLeuYThHISThrAglIeHISerGlyGluYs 600  
 DB 1479 GCCAGATTCAACCGGCGACCACTGAAAAACCACTGAAATTCACCTGAGAGAG 1420  
 QY 601 ProTyrIleGlyGluThrGlyGluYValAaRPhVaGlnValAlaHISLeuAaRAlaHIS 620  
 DB 1419 CCTTACAAATGCGAAACCTGCGAGCAAGATTGTACAGGAGGCGCACTCCGAGCCAT 1360  
 QY 621 ValLeuIleHISThrGlyGluYsProTyrProGlyGluIleGlyGluYThrAaRPhVa 640  
 DB 1359 GTCTTATCCACACTGCTGAGAACCTTATCCCTGTAATCTGTGCAACCCGTTCCGG 1300  
 QY 641 HISLeuGlnThrLeuYsSerHISLeuAaRglIeHISThrGlyGluYsProTyrHIS 660  
 DB 1299 CACCTTCAGACTGGAAGAGCACTGCAATTCACACAGAGAGAAACCTTACCATTTGT 1240  
 QY 661 GluIleGlyAaenLeuHISpHeaRghISLysSerGlnLeuAaRglIeHISLeuAaRglIeYs 680  
 DB 1239 GAGAAAGTGAACCTGCAATTCCTGCAACAAAGCCAGTGCACCTTCACTTGCAGAGAG 1180  
 QY 681 HISglYAlaIleThrAaenThrLysValGlnTyrAaRValSerAlaThrAaRLeuProPro 700  
 DB 1179 CATGGCCGCAATCAACCAACCAAGGTGCAATACCGCTGTCAAGCACTGACCTGCTCCG 1120  
 QY 701 GluLeuProLysAlaCys 706  
 DB 1119 GAGCTCCCAAGCCTGC 1102  
 RESULT 10  
 AAZ90110 ID AAZ90110 standard; cDNA; 3161 BP.  
 XX AC AAZ90110;  
 DT 19-MAY-2000 (first entry)  
 XX DE Human BCL-6 nucleotide sequence.  
 XX DE Bcl-6; human; B-cell lymphoma; regulator; non-Hodgkin's lymphoma;  
 KW diffuse type B-cell lymphoma; ss.  
 XX OS Homo sapiens.  
 XX FH Key location/Qualifiers  
 FT misc\_feature 2687  
 FT /\*tag= a  
 FT /note= "There are approximately 560 additional bases  
 FT present at this position which are undefined in the  
 FT specification"  
 XX W0200000185-A1.  
 XX 06-JAN-2000.  
 XX 30-JUN-1999; 99WO-US014703.  
 XX 30-JUN-1998; 98US-00107058.  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX Dalla-Favera R, Niu H;  
 DR WP1; 2000-150631/14.  
 DR P-PSDB; AAY78792.  
 PT Novel methods for regulating BCL-6 levels in cells used to treat humans  
 PT with lymphoma.  
 PS Example; Fig 9; 15pp; English.  
 CC This sequence represents the human bcl-6 nucleotide sequence. The  
 CC invention relates to a vertebrate bcl-6 locus which is the breakpoint

CC cluster region in B-cell lymphomas, and contains a bcl-6 gene encoding a  
 CC BCL-6 polypeptide. Administration of a molecule which induces  
 CC phosphorylation of BCL-6 and thereby induces BCL-6 degradation, can be  
 CC used as a method of regulating BCL-6 in cells. The methods of the  
 CC invention can be used to regulate, and especially to decrease BCL-6  
 CC levels in cells. The methods may also be used to screen putative  
 CC therapeutic agents for treatment of non-Hodgkin's lymphoma, by contacting  
 CC cells from lymphoma and normal cells with the agent, and after a period  
 CC of time comparing the amount of bcl-6 nucleic acid in each sample, a  
 CC difference indicating the effectiveness of the agent. The bcl-6 gene is a  
 CC source of probes and primers, which are used to diagnose diffuse-type B  
 CC cell lymphoma and B cell lymphoma in a subject. Anti-BCL-6 antibodies may  
 CC also be used for this purpose. The methods are useful for treating non-  
 CC Hodgkin's lymphoma  
 CC XX  
 SQ Sequence 3161 BP; 795 A; 902 C; 766 G; 696 T; 0 U; 2 Other;  
 Alignment Scores:  
 Pred. No.: 4,896-191 Length: 3161  
 Score: 3763.00 Matches: 701  
 Percent Similarity: 99.4% Conservative: 1  
 Best Local Similarity: 99.3% Mismatches: 4  
 Query Match: 99.2% Indels: 0  
 DB: 3 Gaps: 0  
 US-10-755-889-18 (1-706) x AAZ90110 (1-3161)  
 QY 1 MetAlaSerProAlaAaSerGlyIleGlnPheThrAaRghISAlaSerAaRValLeuLeu 20  
 DB 328 ATGGCCTCGCGGCTGACACTGTATCCAGTTCACCGGCATGCCAGGAGATGTTCTTCTC 387  
 QY 21 AsnLeuAaenAaRglLeuAaSerAaRAlaIleLeuThrAaRValIleValIaISerAaR 40  
 DB 388 AACCTTATGCTCTCCGAGATCAAGACATCTTACATGTGATGTGATGTGAGCCCT 447  
 QY 41 GluGlnPheAaRghISLysThrValIleMetAlaCysSerGlyLeuPheYrSerIle 60  
 DB 448 GAGCAGTTTGAAGCCCTTAACACGCTCTCATGCGCTCGAGAGGCCCTGTCTATAGCATC 507  
 QY 61 PheThrAaRglLeuYsCysAsnLeuSerValIleAsnLeuAaRProGluIleAaenPro 80  
 DB 508 TTTACAGACAGTTGAATCAACCTTAGTGATCATCATCTGAGATCAACCT 567  
 QY 81 GluGlyPheCysIleLeuLeuAaRPhMetYrThrSerAaRglLeuAaRglGly 100  
 DB 568 GAGGATTCGACATCCCTCGACCTTCATGATACATCTGCGCTCAATTTGCGAGAGGC 627  
 QY 101 AsnIleMetAlaValMetAlaThrAlaMetYrLeuGlnMetGluHISValIaISerThr 120  
 DB 628 AACATCATGGCTGTGATGGCCAGCGCTATGACTGAGATGGAGATGTTGTGACACT 687  
 QY 121 CysAaRghPheIleYsAlaSerGluAlaGluMetValSerAlaIleYsProProAaR 140  
 DB 688 TGCCGGAAGTTTATTAAGCCAGTGAAGAGAGATGTTTCTGCCATCAAGCCTCTCTGT 747  
 QY 141 GluGlnPheLeuAaenSerAaRMetLeuMetProGlnAaRAlaIleMetAlaYrAaRglYAaR 160  
 DB 748 GAAGAGTTCTTCAACACCGGATGCTGATGCCCAACATCAATGAGGCTTACGAGGCTGT 807  
 QY 161 GluValValGluAaenAaenLeuProLeuAaRSerAlaProGlyCysGluSerAaRAlaPhe 180  
 DB 808 GAGGTGTGAGAAACCTGCACTGAGAGAGCCCTTGAGTGTGAAGAGAGAGCTTT 867  
 QY 181 AlaProSerLeuYrSerGlyLeuSerThrProProAlaSerYrSerMetYrSerHIS 200  
 DB 868 GCCCCAGCCGTGATGAGTGGCTGTCCACACCGCAGCCTTATTCATATCAAGCAC 927  
 QY 201 LeuProValSerSerLeuLeuPheSerAaRglGluLeuAaRValAaRMetProVal 220  
 DB 928 CTCCCTGACAGACCTCTCTCTTCGAGTGAAGAGATTTCCGAGATGTCGAGATCCCTGTG 987  
 QY 221 AlaAaenProPheProLysAlaAaRAlaLeuProCysAaRSerAlaAaRProValProGly 240

Db 988 GCCAACCCCTTCCCAAGGAGCGGCACTCCCATGTGATGTGCGCAGCCAGTCCCTGCT 1047  
 Qy 241 GUTYSSerArgProThrIleuGluValSerProAsnValCysHisSerAsnIleTyrSer 260  
 Db 1048 GAGTACAGCCGGCGGCTTGGAGGTGTCCCAAGTGTGCGACAGCAATATCTATTCA 1107  
 Qy 261 ProLYeGIuThrIleProGluGluAlaArgSerAspMetHisTyrSerValAlaGluGly 280  
 Db 1108 CCCAGGAAACAATCCCAAGAGGCAACAAGTGAATGACATCACTACAGTGTGCTAGGGC 1167  
 Qy 281 LeuLYeProlAlaIleProSerAlaArgAsnAlaProTyrPheProCysAspIleAlaSer 300  
 Db 1168 CTCAAACTGTCTGCCCCCTCAGGCCCAAAATGCCCTTACTCTTCTGTGACAAGGCCACG 1227  
 Qy 301 LYeGIuGluGluArgProSerSerGluAspGluIleAlaLeuHisIlePheGluProProAsn 320  
 Db 1228 AAAAGAAAGAGAGACCTCTCTCGAAGATGAGATTGCCCTGATTTTCAGACCCCAAT 1287  
 Qy 321 AlaProLeuAsnArgLYeGlyLeuValSerProGlnSerProGlnLYeSerAspCysGln 340  
 Db 1288 GCACCCCTGAACCGGAAGGGTGTGTTAGTCCACAGGCCCCCAAAATCTGACTGCCAG 1347  
 Qy 341 ProAsnSerProThrGluAlaCysSerSerLYeAsnAlaCysIleLeuGlnAlaSerGly 360  
 Db 1348 CCCAACTCGCCACAGAGGCTGACAGCAATAGATGCTGATCTCCAGGGGTCTGGC 1407  
 Qy 361 SerProProAlaLYeSerProThrAspProLYeAlaCysAsnTyrLYeTyrLYePhe 380  
 Db 1408 TCCCTTCACAGCCCAAGGCCCTGACCCCAAGCCCTGACGCTGAGAAATCAAGTTTC 1467  
 Qy 381 IleValIleuAsnSerLeuAsnGlnAlaAsnAlaLYeProGlyLYeProGluGlnAlaGluLeu 400  
 Db 1468 ATGTGTCTCAACAGCTCAACCAAGATGCCAAACCAAGGGGGCTGAGAGCTGAGCTG 1527  
 Qy 401 GLYArgLYeSerProArgAlaTyrThrAlaProProAlaCysGlnProMetGluPro 420  
 Db 1528 GGGCGGCTTTCCCAAGAGCTTACAGGCCCACTGAGCTGCGCAGCAACCCATGAGAGCT 1587  
 Qy 421 GlnAsnLeuAspLeuGlnSerProThrLYeLeuSerIleAsnIleGluAspSerThrIle 440  
 Db 1588 GAGAACTTGAACCTTCACTGCTCCCAACCAAGCTGAGCGCAGGGAGGACTCCACCATC 1647  
 Qy 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460  
 Db 1648 CCAACAGCCAGCGGCTCAATACATGTTTAAAGGTTCATGACGGCTCTCCCGCAGC 1707  
 Qy 461 SerSerGluSerHisSerProLeuTyrMetHisIleProProLYeCysThrSerCysGlySer 480  
 Db 1708 AGCAGGAGAGGCACTCACACTTACATGACCCCCCAAGTGCAGCTCTCGGCTCT 1767  
 Qy 481 GlnSerProGlnHisAlaGluMetCysGluHisIleThrAlaGlyProThrPheAlaGluGln 500  
 Db 1768 CAGTCCCAACAGATGAGAGATGTGCTCCACACCCCTGCCCCCAAGTTCGTGAGAG 1827  
 Qy 501 MetGlyGluThrGlnSerGluTyrSerAspSerSerCysGluAsnGluAlaPhePheCys 520  
 Db 1828 ATGGAGAGAGCCCACTGAGTACTCAGATTCTAGCTGTAGAAACGGGGCTTCTTCTGC 1887  
 Qy 521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLYeAsnArgHisIleLeuGlnThr 540  
 Db 1888 AATGAGTGTAGTCCGCTTCTCTGAGAGGCGCTCACTCAAGAGGCAACAGCTGCAGACC 1947  
 Qy 541 HisSerAspLYeProTyrLYeCysAspArgCysGlnAlaSerPheArgTyrLYeGlyAsn 560  
 Db 1948 CACAGTACAAACCTTCAAGTGTGACCGCTGCAGGCCCTTCCCTCAAGAGGGCAAC 2007  
 Qy 561 LeuAlaSerHisLYeThrValHisIleThrGlyGluLYeProTyrArgCysAsnIleCysGly 580  
 Db 2008 CTGCGCCAGCCCAAGACCGTTCATACCGGTGAGAAACCTTACTTCTTCAACATCTGTGG 2067  
 Qy 581 AlaGlnPheAsnArgProAlaAsnLeuLYeThrHisIleThrArgIleHisSerGlyGluLYe 600  
 Db 2068 GCCCAGTTCAACGGCGCAGGCAACTGAAAAACCACTGAATTCACTGTGAGAGAGAG 2127

Qy 601 ProTyrLYeCysGluThrCysGlyAlaArgPheValGlnValAlaHisIleLeuArgAlaHis 620  
 Db 2128 CCTTCAATGCGAAATCGCGAGCCAGATTTGTATACAGGTGGCCACCTCGTCCCAT 2187  
 Qy 621 ValIleuIleHisIleThrGlyGluLYeProTyrProCysGluIleCysGlyThrArgPheArg 640  
 Db 2188 GTGCTTATCCACACTGTGTAGAGAGCCCTATGCTGTGAATCTGTGGACCCGGTTCCGG 2247  
 Qy 641 HisLeuGlnThrLeuLYeSerHisIleuArgIleHisIleThrGlyGluLYeProTyrHisCys 660  
 Db 2248 CACCTTCAGACTTGAAGAGCCACTGGCAATCCACAGAGAGAAACCTTACCATTTGT 2307  
 Qy 661 GlnLYeCysAsnLeuHisPheArgHisLYeSerGlnLeuArgLeuHisIleuArgGlnLYe 680  
 Db 2308 GAGAACTGATACCTTCATTTCCGTACAAAGCCAGCTGCGACTTCACTGTGCGCAAG 2367  
 Qy 681 HisGlyAlaIleThrAsnThrLYeValGlnTyrArgValSerAlaThrAspLeuProPro 700  
 Db 2368 CATGGCGCATCACCAACCAAGGTGCAATGCCGCTGTGAGCCAGCTGACTGCTCG 2427  
 Qy 701 GlnLeuProLYeAlaCys 706  
 Db 2428 GAGCTCCCAAGCCTGC 2445  
 RESULT 11  
 AA080513  
 ID AA080513 standard; cDNA; 3720 BP.  
 AC AA080513;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 19-JUL-1995 (first entry)  
 XX  
 DE Genetic locus bcl-6.  
 XX  
 KW bcl-6 locus; non-Hodgkin lymphoma; B-cell lymphoma; B-lymphocyte;  
 KW diagnostic; therapeutic; chromosome-3q27; translocation; proto-oncogene;  
 XX  
 OS diffuse large cell lymphoma; DCL; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 328..2448  
 FT /\*tag= a  
 FT misc\_difference 2687..3246  
 FT /\*tag= b  
 FT /note= "base n at positions 2687-3246 are not identified  
 FT in the specification"  
 XX  
 PN MO9429343-A1.  
 XX  
 PD 22-DEC-1994.  
 XX  
 PF 09-JUN-1994; 94MO-US006669.  
 XX  
 PR 09-JUN-1993; 93US-00074967.  
 XX  
 PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA (SLOK ) SLOAN KETTERING INST CANCER.  
 XX  
 PI Dalla-Favera R, Chaganti RS;  
 DR WPI; 1995-036403/05.  
 DR P-PSDB; AARE8743.  
 XX  
 PT Nucleic acid from genetic locus bcl-6 - used to develop prods. for  
 PT diagnosis and therapy of B-cell lymphoma and non-Hodgkin's lymphoma.  
 XX  
 PS Disclosure, Page 90-94; 129pp; English.  
 XX  
 CC DNA was extd. from tumor tissue of 2 cases of IgM-producing diffuse-type  
 CC B-cell NHL carrying the t(3;14)(q27;q32) translocation. DNA analysis



Db 2188 GTGCTTATCOACACGTGTGAGAACCCCTATCCCTGTGAATCTGTGGACCCGTTCCGG 2247  
 Qy 641 HsLeuGlnThrLeuLysSerHisLeuAlaGlyHisThrGlyGluLysProGlyThrSerCys 660  
 Db 2248 CACCTTCAGACTCTGAGAGCCACCTGCAGATCCACAGAGAGAAACCTTACCACTTGT 2307  
 Qy 661 GluLysCysAsnLeuHisPheArgHisLysSerGlnLeuArgLeuHisLeuArgGlnLys 680  
 Db 2308 GAGAAAGTGAACCTGCACTTCCCTGCACAAAGCCAGCTGCAGCTTCACTTGGCCAGAG 2367  
 Qy 681 HsGlyAlaAlaLeuThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700  
 Db 2368 CATGGCGGCATCAACCAACCAAGTGCATATCCGCGTGCAGCCACTGACCTGCTCCG 2427  
 Qy 701 GluLeuProLysAlaCys 706  
 Db 2428 GAGCTCCCCCAAGCCTGC 2445  
 RESULT 12  
 ABI99745  
 ID ABI99745 standard; cDNA; 2373 BP.  
 AC ABI99745;  
 XX 07-MAR-2002 (first entry)  
 DT Mouse ischaemic condition related cDNA sequence SEQ ID NO:813.  
 DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:813.  
 XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
 KM vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.  
 XX Mus musculus.  
 OS Mus musculus.  
 XX WO200188188-A2.  
 PN 22-NOV-2001.  
 PD 18-MAY-2001; 2001WO-JP004192.  
 PF 18-MAY-2000; 2000JP-00145977.  
 PR 18-MAY-2000; 2000JP-00145977.  
 XX (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
 PA Ishikawa K, Arai S, Takahashi Y, Nagata T, Ishii Y;  
 PI Ishikawa K, Arai S, Takahashi Y, Nagata T, Ishii Y;  
 DR WPI; 2002-034733/04.  
 DR P-PSDB; ABB57289.  
 XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
 PT expression levels of particular genes defined in the specification or by  
 PT determining the expression profile of a gene group comprising these  
 PT genes.  
 XX Claim 2; Page 1999-2003; 2690BP; English.  
 XX The present invention describes a method for examining ischemic  
 CC conditions, comprising measuring the expression levels of particular  
 CC genes (I) in a test sample or determining the expression profile of a  
 CC gene group in the sample comprising genes selected from (I). The method  
 CC is useful for examining the ischemic condition (e.g. compressive  
 CC ischemia, occlusive ischemia or vasospastic ischemia) by measuring the  
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding the  
 CC protein sequences in ABB57020 to ABB57374) or by determining the  
 CC expression profile of a gene group comprising these genes. The expression  
 CC levels or expression profiles produced by these genes are used as an  
 CC indicator when screening for ischemic condition-improving drugs or  
 CC therapeutics for ischemic diseases. ABI99913 and ABI99914 represent PCR  
 CC primers for a mouse ischaemic condition related sequence, which are used  
 CC in the exemplification of the present invention  
 XX Sequence 2373 BP; 566 A; 745 C; 574 G; 488 T; 0 U; 0 Other;  
 SQ Alignment Scores:

Pred. No.:	1,246-182	Length:	2373
Score:	3602.50	Matches:	666
Percent Similarity:	96.2%	Conservative:	14
Best Local Similarity:	94.2%	Mismatches:	26
Query Match:	95.0%	Indels:	1
DB:	6	Gaps:	1

US-10-755-889-18 (1-706) x ABI99745 (1-2373)  
 Qy 1 MetAlaSerProAlaAspSerCysLeuGlnPheThrArgHisAlaSerAspValLeuLeu 20  
 Db 101 ATGGCTCCCGCGCTGACAGAGCTGATCCAGTTTACCGGACGCTAGTGAATGTTCTTC 160  
 Qy 21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValIleValIleSerArg 40  
 Db 161 AACCTTATCGCTCCGAGTGGAGTGGACATCTTGACGAGAGTTGTGATGATGGTGGAGCCGT 220  
 Qy 41 GluGlnPheArgAlaHisLysThrValLeuMetAlaCysSerGlyLeuPheTyrSerIle 60  
 Db 221 GAGCAGTTTAGAGCCCATAGACAGTGCATAGCCTCAGCGCTGACGCGCTTCTTACAGTATC 280  
 Qy 61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80  
 Db 281 TTCCTGACCAAGTTGAATGACACCTTAGTGAATCAATGATGCTGAATTCAGCCCT 340  
 Qy 81 GluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100  
 Db 341 GAGGGCTTTGCACTCTCTCTGACATTCATGACATCTGAGCTCAACTGAGGAGAGCC 400  
 Qy 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValIleAspThr 120  
 Db 401 AATATCATGGCGGTATGACACACAGCCATGTACCTGACGATGAGCATGTTGTGACACA 460  
 Qy 121 CysArgLysPheIleLysValSerGluValGlnMetCysIleLeuSerProProArg 140  
 Db 461 TCGAGGAATTCATCAAGGCGCAGTGAAGAGAAATGGCCCTGCACTTAACTCCCTCCCT 520  
 Qy 141 GluGluPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160  
 Db 521 GAAAGTCTCTGAACAGCCGAGATGCTGATGCCCATGACATCATGAGCCATCCGAGGTGCT 580  
 Qy 161 GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe 180  
 Db 581 GAGGTGTGTGAACAATATGCTGACCTGAGAAATATCTCCGCGGTGTGAGAGAGCTTTT 640  
 Qy 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200  
 Db 641 GCTCTCTCTGTATCAGTGGCTGTGTCACACACAGCCTTTATTCCTCCATGTACAGCCAT 700  
 Qy 201 LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspVal---ArgMetPro 219  
 Db 701 CTCCCGCTCAGACCTTCTCTCTCTCTGATGAGAGCTCCGAGATGCCCCCGAGATGCTT 760  
 Qy 220 ValAlaAsnProPheProLysGluArgAlaLeuProCysAspSerAlaArgProValPro 239  
 Db 761 GTGGCCCAACCTTTTCCCAAGAGAGCGTCCCTCCCTGAGACAGTGGCCAGGAAAGTCCCT 820  
 Qy 240 GlyGluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyr 259  
 Db 821 AATGATTAATAGACAGGCGACCATGAGGTGCCCAAGTTGTGTACAGCAACATCTAC 880  
 Qy 260 SerProLysGluThrIleProGluGluAlaArgSerAspMetHisTyrSerValAlaGlu 279  
 Db 881 TCGCCCAAGAGGACGTCCCAAGAGAGGCTCGAGATGACATACATCACTGAGTGGCTGAG 940  
 Qy 280 GlyLeuLysProAlaIleProSerAlaArgAsnAlaProTyrPheProCysAspLysAla 299  
 Db 941 GCGCCCAAGCTGTCTCTCTCTGCTCGAATGCTCCATATCTCCCTGTGACAAAGCC 1000  
 Qy 300 SerLysGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProPro 319  
 Db 1001 AGCAAGAAGAGAGAGACCTTCTTGTGAGAGATGAGATTTGCCCTGATTCGAGCCCTCC 1060

QY 320 AsnAlaProLeuAenArglySGlyLeuValSerProGlnSerProGlnLysSerAspCys 339  
 DB 1061 AATGACACCTTGAAACCGAAGAGGTCTGTTAGTCCAGAGTCCCGAATTCGACTGC 1120  
 QY 340 GlnProAenSerProThrglnAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSer 359  
 DB 1121 CAGCCCAACTCACCAAGAGTCTTGACAGCAGCAAGAGTCTGCTTCAAGGCTCT 1180  
 QY 360 GlySerProProAlaLysSerProThrAspProLysAlaCysAsnTrpLysLeuVal 379  
 DB 1181 GGCTCTCGGACGAGCAAGAGCCCGAAGAGCTGCACTGGAAGAGATPAG 1240  
 QY 380 PheIleValLeuAenSerLysAsnGlnAsnAlaLysProGlyGlyProGlnGlnAlaGlu 399  
 DB 1241 TTCATGCTTTCACACAGCTTCATACAGATTCGCAAAACCGAGGCTCTGACAGACGAG 1300  
 QY 400 LeuAlaLysLeuSerProArgAlaLysThrAlaProProAlaCysGlnProProMetGlu 419  
 DB 1301 CTGGGTGGCTCTCCCTCGAGCTTACCTGACACCGCCCTTGCCAGCCGCTATGAG 1360  
 QY 420 ProGlnAenLeuAenAspLeuGlnSerProThrLysLeuSerAlaSerGlyLysAspSerThr 439  
 DB 1361 CCGCGAAGACTTGAATCTCCACTCCCGACAGCTCAGTGCAGTGGGAGAGACTTACC 1420  
 QY 440 IleProGlnAlaSerArgLeuAenAsnIleValAenArgSerMetThrGlySerProArg 459  
 DB 1421 ATCCCCCAAGCAGCCGGCTCATATATCTCTGAAACAGTCTCTGGAGGCTCCCGCCGA 1480  
 QY 460 SerSerSerGlnSerLysSerProLeuTrpMetHisProLysCysThrSerGlyGly 479  
 DB 1481 AGCAGCAGTGAAGTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1540  
 QY 480 SerGlnSerProGlnHisAlaGlnMetCysLeuHisThrAlaGlyProThrPheAlaGlu 499  
 DB 1541 TCTCAGTCCCAACAGCATACAGATGTGCTTCAATATGCTGGGCGCACGCTCCCGAG 1600  
 QY 500 GlnMetGlyGlnThrglnSerGlnLysSerAspSerSerCysGlnAsnGlyAlaPhePhe 519  
 DB 1601 GAGATGGGGGAAACCCAGTCAAGATTTCCGATTTCTACCTGTGAGAAATGGGACCTTCTTC 1660  
 QY 520 CysAsnGlnCysAspCysArgPheSerGlnGlnAlaSerLeuLysArgHisThrLeuGln 539  
 DB 1661 TGCAACGATGTGATGCTGCTTCTGAGAGGCTGCTCAAGAGCAGCAGCTGAG 1720  
 QY 540 ThrHisSerAspLysProTrpLysCysAspArgCysGlnAlaSerPheArgTrpLysGly 559  
 DB 1721 ACGCACTGACAAACATACAAATGTATGCTGCCAGGCTCTTCCGCTACAAAGGC 1780  
 QY 560 AsnLeuAlaSerHisLysThrValHisThrGlyGlnLysProTrpArgCysAsnIleCys 579  
 DB 1781 AACCTCGCAGCAGCAAGACTGTCCACAGGCTGAGAAACCTTATCGCTGTACATTGT 1840  
 QY 580 GlnAlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgIleHisSerGlyGlu 599  
 DB 1841 GGAGGCGAGTTCAAATCGGCGAGCCCACTGAGACCACTCGAATTCACCTGAGAA 1900  
 QY 600 LysProTrpLysCysGlnThrglnCysGlnAlaArgPheValGlnValAlaHisLeuArgAla 619  
 DB 1901 AAGCCCTCAATGTGAACCTGTGGGCGAGGTTGTTCAGTGGCCCACTCCGTGCC 1960  
 QY 620 HisValLeuIleHisThrGlyGlnLysProTrpCysGlnIleCysGlyThrArgPhe 639  
 DB 1961 CACGTGCTCATTCACACTGAGAGAGAGCGTACCCCTGTGAATCTGTGGCAGCTGCTTC 2020  
 QY 640 ArgHisLeuGlnThrglnLysSerHisLeuAlaGlnIleHisThrGlyGlnLysProTrpHis 659  
 DB 2021 CGGCACTTCACAGCTCTGAGAGGCAATCGCATTCACAGAGAGAGAAACCTTACAT 2080  
 QY 660 CysGlnLysCysAsnLeuHisPheArgHisLysSerGlnLeuArgLeuHisLeuArgGln 679  
 DB 2081 TGTGAGAACTGTAACTGCACTTGTCTCAAAAGCCAACTGCACTTATTTGGGCCAG 2140  
 QY 680 LysHisGlyAlaIleThrAsnThrLysValGlnTrpArgValSerAlaThrAspLeuPro 699

DB 2141 AAGCAGCGGCGCATTCACAAACACCAAGTGCATACGCGTGTGGCGCTGACCTGCT 2200  
 QY 700 ProGlnLeuProLysAlaCys 706  
 DB 2201 CCGAGCTCCCAAGGCTGC 2221  
 RESULT 13  
 ADEL13839  
 ID ADEL13839 standard; DNA; 1440 BP.  
 AC ADEL13839;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE AAC2-2 nucleotide sequence SEQ ID NO:2.  
 XX  
 KM carcinomaembryonic antigen; CEA; CEA(6D)-1; 2; cytostatic; vaccine; cancer;  
 KM tumour antigen; immunotherapy; angiogenesis-associated antigen; AAC2-2;  
 KM gene; ds.  
 XX  
 OS unidentified.  
 XX  
 PN WO2003085087-A2.  
 PD 16-OCT-2003.  
 XX  
 PF 09-APR-2003; 2003WO-US010916.  
 XX  
 PR 09-APR-2002; 2002US-0372972P.  
 XX  
 PA (AVET ) AVENTIS PASTEUR LTD.  
 PA (THER-) THERION BIOLOGICS INC.  
 PI Parrington M, Zhang L, Rovinski B, Griz LR, Greenhalgh T;  
 XX  
 DR WPI: 2003-877029/81.  
 XX  
 PT New isolated DNA molecule comprising the carcinomaembryonic antigen (6D)-  
 PT 1,2 sequence, useful for diagnosing, preventing and treating cancer, or  
 PT determining the effectiveness of a chemotherapeutic or other treatment  
 PT regimen.  
 XX  
 PS Disclosure; SEQ ID NO 2; 56bp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule comprising the  
 CC carcinomaembryonic antigen (CEA) (6D)-1,2 sequence of 2106 bp (see  
 CC ADEL13861), or its fragment. Also described: (1) an expression vector  
 CC comprising the nucleic acid sequence CEA(6D)-1,2, or its fragment  
 CC describing above; (2) a composition comprising the expression vector of  
 CC (1) in a pharmaceutical carrier; and (3) preventing or treating cancer  
 CC comprising administering to a host the expression vector of (1). CEA(6D)-  
 CC 1,2 has cytostatic activity, and can be used in vaccines. The CEA(6D)-1,2  
 CC nucleic acid and target polypeptide are useful for diagnosing, preventing  
 CC and treating cancer, predicting prognosis, or determining the  
 CC effectiveness of a chemotherapeutic or other treatment regimen. The  
 CC expression vector may be used for the insertion and expression of CEA(6D)-  
 CC 1-2 nucleic acid encoding tumour antigens for the immunotherapeutic  
 CC treatment of cancer. The target polypeptides are useful in generating  
 CC antibodies used in screening assays or for immunotherapy. The present  
 CC sequence represents the angiogenesis-associated antigen AAC2-2, which is  
 CC given in the exemplification of the present invention.  
 XX  
 SQ Sequence 1440 BP; 300 A; 503 C; 381 G; 256 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.21e-52 Length: 1440  
 Score: 1155.00 Matches: 268  
 Percent Similarity: 46.6% Conservative: 58  
 Best Local Similarity: 38.3% Mismatches: 142  
 Query Match: 30.5% Indels: 232  
 DB: 10 Gaps: 15



US-10-755-889-18 (1-706) x ADEI3839 (1-1440)

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QY 1 MetAlaSerProIla-----AspSerCysIle-----GlnPheThrArgHis 14
Db 1 ATGGGTTCCTCCCGCCCGAGGAGGAGCGCTGGGCTACGTCGCGAGTTCACCTCCGAC 60
QY 15 AlaSerAspValIleuLeuAenLeuAenAargLeuArgSerArgAspIleLeuThrArgVal 34
Db 61 TCTTCGAGACGTCGTCGGGCAACCTCAACGAGCTGCGTCGGGATCTCTCACTGACGTC 120
QY 35 ValIleValIaSerArgIugIugIugIugIugIugIugIugIugIugIugIugIugIug 54
Db 121 ACCGCTGCTGGTGGCGGCAACCCCTCAGACGACACAGGCAAGTTCATTCGCTCGAGT 180
QY 55 GlyLeuPheThrSerIlePheThrArgGlnLeuLeuLeuLeuLeuLeuLeuLeuLeu 74
Db 181 GGGCTTCTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 240
QY 75 AspProGluIleAenProGluIugIugIugIugIugIugIugIugIugIugIugIug 94
Db 241 CCGGGGGGTCCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
QY 95 LeuAenLeuArgIugIugIugIugIugIugIugIugIugIugIugIugIugIugIug 114
Db 301 CTGGGCTCTCTCCAGGCACTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 115 GlnHisValIaSerArgIugIugIugIugIugIugIugIugIugIugIugIugIug 134
Db 361 GAGCAGCTGGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 402
QY 135 AlaIleArgProArgIugIugIugIugIugIugIugIugIugIugIugIugIug 154
Db 402 ----- 402
QY 155 MetAlaTyArgIugIugIugIugIugIugIugIugIugIugIugIugIugIugIug 174
Db 402 ----- 402
QY 175 CysGluSerArgIaPheAlaProSerLeuTySerGlyLeuSerThrProProAlaSer 194
Db 402 ----- 402
QY 195 TyrSerMetTyrSerHisLeuProValSerSerLeuPheSerAspGluIugPheArg 214
Db 403 ----- 403
QY 215 AspValaArgMetProValaIaAenProPheProLeuGluArgIaLeuProCysAspSer 234
Db 423 ----- 423
QY 235 AlaArgProValaProGluGluTyrSerArgProThrLeuGluValSerProAenValaCys 254
Db 423 ----- 423
QY 255 HisSerAenIleTyrSerProLeuGluThrIleProGluGluIaArgSerAspMetHis 274
Db 423 ----- 423
QY 275 TyrSerValaIaGluGluLeuLeuPheProAlaIaProSerAlaArgAenAlaProTyrPhe 294
Db 424 ----- 424
QY 295 ProCysAspIyAsaIaSerIyGluGluGluGluGluGluGluGluGluGluGluGlu 314
Db 436 ----- 436
QY 315 HisPheGluProProAenAlaProLeuAenArgIyGlyLeuValSerProGlnSerPro 334
Db 454 ----- 454
QY 335 GlnIySerAspCysGlnProAenSerProThrGluIaCysSerSerIyAsnAlaCys 354
Db 484 AGGGGCTCCGAGAGACCCAGACCACTAATCTGAAGC----- 528
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QY 355 IleLeuGlnAlaSerGlySerProProAlaIySerSerProThrAspProIyValaCysAen 374
Db 529 ----- 529
QY 375 TrpIySerTyrIyPheIleValaLeuAenSerLeuAenGlnAenAlaIySerProGluGly 394
Db 580 TGGAAAGAGTCAAGATACATCTGCTAAATCT----- 612
QY 395 ProGluGlnAlaGluLeuGluIyArgLeuSerProArgAlaIyThrThAlaProProAlaCys 414
Db 613 ---CAGGCTCCCAAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 669
QY 415 GlnProProMetGluProGluAenLeuAenLeuAenLeuAenLeuAenLeuAenLeu 434
Db 670 CAAGCAGAGCTCCCAAGTGAAGACAGGCTCCAGACAGGAGGAGGAGGAGGAGGAGG 729
QY 435 GlyIuAspSerThrIlePro---GlnAlaSerArgLeuAenAenIleValaIenArgSer 453
Db 730 AGTGAAGAAGAACCATTCCTGCTCCAGACAGGCTC----- 768
QY 454 MetThrIySerProArgSerSerSerGluSerHisSerProLeuTyThrMetHisProPro 473
Db 769 ----- 795
QY 474 TySerThrSerCysGlySerGlnSerProGlnHisAlaGluMetCysLeuHisThrAla 493
Db 796 ----- 840
QY 494 GlyProThrPheAlaGluIugIugIugIugIugIugIugIugIugIugIugIugIug 513
Db 841 ----- 888
QY 514 GluAenGlyAlaPhePheCysAenGluCysAspCysArgPheSerGluIugIuAlaSerLeu 533
Db 889 GGAAGGAATTTTTCAGCTGCAAGACGTGAGGCTGGGAGGAGGAGGAGGAGGAGGAGG 948
QY 534 TyArgHisThrLeuGlnThrHisSerAspIyProTyrIyCysAspArgCysGlnAla 553
Db 949 GAC---TCCTTGCTTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1005
QY 554 SerPheArgTyrIyGlyIyAenLeuAlaSerHisIyLeuThrValHisThrGlyIugIyPro 573
Db 1006 TCGTTCGCTTCAAGGAGCACTTGCAGTCACTGTAAGTCACTGTCGCTGCGGCT 1065
QY 574 TyrArgCysAenIleCysGlyIyAenPheAenArgProAlaAenLeuTyThrHisIstr 593
Db 1066 TACCACTGCTCAATCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1125
QY 594 ArgIleHisSerGlyIyIyIyProTyrIyCysGluThrCysGlyAlaIaArgPheValaGln 613
Db 1126 CGGATCAATTCGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1185
QY 614 ValAlaHisLeuArgAlaHisIyValIleuIleHisThrGlyIyIyProTyrProCysGlu 633
Db 1186 GTGGACATCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1245
QY 634 IleCysGlyThrArgPheArgHisIleuGlnThrIleLeuLeuSerHisIleuArgIleHisIstr 653
Db 1246 ACCCTGGAGAACCGGCTTCGCGACCTGACAGACCTTAAGAGCCACCTTGACATCCACCC 1305
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Db 1306 GAGAGAGAGCTTACATTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1365
QY 674 ArgLeuHisLeuArgGluIyIyIyIyAlaIleThrAsnThrIyValGlnTyrArgVal 693
Db 1366 CGGCTCATCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1425
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RESULT 14  
AAL56278  
ID AAL56278 standard; DNA; 1440 BP.  
XX





QY 454 MetThrGlySerProArgSerSerGlnSerHisSerProLeuTyrMetHisProPro 473  
 DB 769 -----TCTCAACTGCTGCACTGTCAGTTC----- 795  
 QY 474 LysCysThrSerCysGlySerGlnSerProGlnHisAlaGluMetCysLeuHisThrAla 493  
 DB 796 -----AAATGTGG-----GCTCCAGCCAGTACCCCTCATCTCATCATCCAG 840  
 QY 494 GlyProThrPheAlaGluMetGlyGluThrGlnSerGluTyrSerHisSerSerCys 513  
 DB 841 -----GCTCAGACACCTCTGATCAGTCCCTGTAACAGGCTGCTCCATCCAG 888  
 QY 514 GluAsnGlyAlaPhePheCysAsnGluCysAspCysArgPheSerGlnGluAlaSerLeu 533  
 DB 889 GGAAGTGAATTTTTCAGCTCCAGAACTGTAGAGCTGTGACAGGCTCATCGGGCTG 948  
 QY 534 LysArgHisThrLeuGlnThrHisSerAspLysProTyrLysCysAspArgCysAla 553  
 DB 949 GAC---TCTTGGTTCCTGGGAGCAAGAACCCCTATAGTCACTGTCGGCTCT 1005  
 QY 554 SerPheArgTyrLysGlyAsnLeuAlaSerHisLysThrValHisThrGlyGluPro 573  
 DB 1006 TCGTCCGCTACAAAGGCACTTGGCCATCTCATCTGACACAGGGGAAAAGCCT 1065  
 QY 574 TyrArgCysAsnLysCysGlyAlaGlnPheAsnArgProAlaAsnLeuLysThrHis 593  
 DB 1066 TACCACTGCTCAATCTGGAGAGCCGCTTTAACCGGCAAGAACCTGAAGACGACAGC 1125  
 QY 594 ArgIleHisSerGlyGlyLysProTyrLysCysGlyLysThrCysGlyAlaArgPheVal 613  
 DB 1126 CGCATTCATTCGGAGAGAACCCGTTAAGTGAAGACGTCGGCTCGGCTTTGTAACG 1185  
 QY 614 ValAlaHisLeuArgAlaHisValLeuIleHisThrGlyGluLysProTyrProCysGlu 633  
 DB 1186 GTGGCAATCTGGCGGCGACGTCGTGATCCACACCGGAGAGACCCCTACCTTGCCCT 1245  
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 DB 1306 GGAAGAAAGCTTACCACTGGACCCCTGTGGCTGATTTCCGGACAAAGTCAACTG 1365  
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 DB 1366 CGGCTGATCTGGCCGAGAAACAGGAGCTGCTACAAACCAAAAGTCACTACCACTT 1425  
 RESULT 15  
 ADU99230 standard; DNA, 1440 BP.  
 ID ADU99230  
 XX AC ADU99230;  
 XX 24-FEB-2005 (first entry)  
 DE AAC2-2 tumor-associated antigen open reading frame - SEQ ID 4.  
 XX expression vector; tumor-associated antigen; cancer; cytostatic; gene;  
 KM des; AAC2-2.  
 OS Unidentified.  
 XX  
 OS  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 1..1440  
 FT /\*tag= a  
 FT /product= "AAC2-2 tumor-associated antigen - SEQ ID 5"  
 XX  
 XX MO2004104039-A2.  
 XX 02-DEC-2004.  
 XX 15-MAY-2004; 2004WO-US015202.

XX  
 PR 16-MAY-2003; 2003US-0471119P.  
 PR 16-MAY-2003; 2003US-0471193P.  
 XX  
 PA (AVERT ) AVENTIS PASTEUR INC.  
 XX  
 PI Bernstein N, Galliehan S, Lovlett C, Parrington M, Radvanyi L,  
 PI Singh-Sandhu D,  
 XX  
 DR WPI; 2004-834272/82.  
 DR P-PSDB; ADU99231.  
 XX  
 PT New expression vector comprising a nucleic acid encoding a tumor antigen,  
 PT e.g. BFA4, BGY1, BFA5, BC24, or BGY3, useful for expressing multiple  
 XX tumor antigens, or for preventing or treating cancer.  
 XX  
 PS Disclosure; SEQ ID NO 4; 109pp; English.  
 XX  
 CC The invention comprises an expression vector that contains a nucleic acid  
 CC encoding a tumor antigen (e.g. BC24 or BGY3). The expression vector of  
 CC the invention is useful for the expression of multiple tumor antigens and  
 CC the prevention or treatment of cancer. The present DNA sequence encodes  
 CC the AAC2-2 tumor-associated antigen.  
 XX  
 SQ Sequence 1440 BP; 300 A; 503 C; 381 G; 256 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1,21e-52 Length: 1440  
 Score: 1155.00 Matches: 268  
 Percent Similarity: 46.6% Conservative: 58  
 Best Local Similarity: 38.3% Mismatches: 142  
 Query Match: 30.5% Indels: 232  
 DB: 13 Gaps: 15  
 US-10-755-889-18 (1-706) x ADU99230 (1-1440)  
 QY 1 MetAlaSerProAla-----AspSerCysIle-----GlnPheThrArgHis 14  
 DB 1 ATGGTTCCTCCCGCGCGCGCGAGGAGCGCTGAGGCTACGCGGAGTTCACCTCGCCAC 60  
 QY 15 AlaSerAspValLeuLeuAsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspVal 34  
 DB 61 TCTCCGAGAGTCTGGGCAACTCAACGAGCTGCGCTGCGGAGTCTCACTGACGTC 120  
 QY 35 ValIleValAlaSerArgGlnGlnPheArgAlaHisLysThrValLeuMetAlaCysSer 54  
 DB 121 ACCTGCTGTGGCGGAGACCCCTCAGAGCACACAGGCAAGTTCCTCATCGCTGCACT 180  
 QY 55 GlyLeuPheTyrSerIlePheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeu 74  
 DB 181 GGCTTCTTCTATTCATTTTCCGGGGCGCTGCGGAGTGGGGGTGACGTCCTCTCTG 240  
 QY 75 AspProGluIleAsnProGluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArg 94  
 DB 241 CCGGGGGGTCCGAGACGAGAGGCTTGGCCCTCTATTGACTTCACTTACACTTGGCCG 300  
 QY 95 LeuAsnLeuArgGlnGluLysenIleMetAlaValMetAlaThrLysMetTyrLeuGlnMet 114  
 DB 301 CTGCGCTCTCTCCACCACTGACACAGAGTCTAGCGGCCGCCCACTATTGTCAGATG 360  
 QY 115 GluHisValAlaAspThrCysArgLysPheIleLysAlaSerGluAlaGluMetValSer 134  
 DB 361 GACCACTGTGTCCAGGACATGCCACCCCTTCATCCAGGCCACG----- 402  
 QY 135 AlaIleLysProProArgGlnGluPheLeuAsnSerArgMetLeuMetProGlnAspIle 154  
 DB 402 ----- 402  
 QY 155 MetAlaTyrArgGlyArgGluValValGluAsnAsnLeuProLeuArgSerAlaProGly 174  
 DB 402 ----- 402  
 QY 175 CysGluSerArgAlaPheAlaProSerLeuTyrSerGlyLeuSerThrProProAlaSer 194

[illegible]

Db 949 GAC---TCCTTGATTCTCGGGAGCAAGACAAACCTATAGTGCAGTGGCGGTC 1005

QY 554 SerPheArgTYLysGlyAsnLeuAlaSerHisLysThrValHisThrGlyGlyLysPro 573

Db 1006 TCGTTCCGCTACAAAGGGCAACCTTGCCAGTCATGTCACAGTCACACAGGGGAAAACCT 1065

QY 574 TYrArgCysAsnIleCysGlyValGlnPheAsnArgProAlaAsnLeuLysThrHisThr 593

Db 1066 TACACATGCTCAATCTGGGAGAGCCGGTTTAAACCGGCACAGCAACCTGAACCAACGACAGC 1125

QY 594 ArgIleHisSerGlyGlyLysProTYrLysCysGluThrCysGlyAlaAsnPheValGln 613

Db 1126 CGCATCCATTCGGAGAGAGAACCCCTATAGTGAAGACGTGGCGCTGCGCTTGTGTACG 1185

QY 614 ValAlaHisLeuAlaGlnHisValLeuIleHisThrGlyGlyLysProTYrProCysGlu 633

Db 1186 GTGGCACATCTGGCGGGCGCACAGTCTGATTCACACCGGGAGGAAGCCCTTACCTTGGCCT 1245

QY 634 IleCysGlyTYrHisArgPheArgHisIleGlnThrLeuLysSerHisIleuArgIleHisThr 653

Db 1246 AACTGCGGAACCCGCTTCGCCCACTTGAGACCTTCAGAGACCAACGTTCCGATCCACACC 1305

QY 654 GlyGlyLysProTYrHisCysGlnLysCysAsnLeuHisPheArgHisLysSerGlnLeu 673

Db 1306 GGAGAGGAAGCCCTTACCACTGCGACCCCTGTGGCTTGCAATTCGGGCACAAAGTCAACTG 1365

QY 674 ArgLeuHisIleuAsnArgGlnLysHisGlyValAlaIleThrAsnThrLysValGlnTYrArgVal 693

Db 1366 CGGCTGCATCTGCGCCAAAGAACGAGACCTGTCACACCAACCAAGTGCATTCACACATT 1425

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Job time : 1172 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

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Title: US-10-755-889-18

Perfect score: 3793  
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Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

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Listing first 45 summaries

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2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gse1:\*  
10: gb\_gse2:\*  
11: gb\_gse3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3760	99.1	2985	4	CR858790 Pongo pyg
2	3604.5	95.0	3307	4	AK039228 Mus muscu
3	3598.5	94.9	3289	4	AK036975 Mus muscu
4	3519	92.8	1977	10	AY399831 Homo sapi
5	3351.5	88.4	1980	10	AY399833 Mus muscu
6	2521	66.5	1702	10	AY399832 Pan trogl
7	1493	39.4	920	5	BX431187 BX431187

8	1446	38.1	859	8	CX565176
9	1395.5	36.8	1092	3	BM550970
10	1381.5	36.4	856	5	BQ722826
11	1362	35.9	1004	3	BM801045
12	1335	35.2	800	1	AJ454603
13	1331.5	35.1	804	5	BQ716058
14	1286	33.9	849	5	BX419860
15	1284	33.9	798	1	AJ441866
16	1274	33.6	830	8	DN285116
17	1262	33.3	867	8	DN286427
18	1248	32.9	690	7	CN401515
19	1215.5	32.0	816	7	CK304021
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21	1187	31.3	995	5	BQ730532
22	1175	31.0	913	3	BQ230532
23	1162	30.6	704	1	AJ398804
24	1157.5	30.5	1425	10	AY415850
25	1154	30.4	772	7	CN401514
26	1151.5	29.0	1443	10	AY415848
27	1132	29.8	840	7	CO573472
28	1113	29.4	736	7	CK957562
29	1109.5	29.3	822	5	BU404010
30	1100.5	29.0	744	3	BU738471
31	1094	28.8	749	1	AJ454600
32	1091	28.8	617	6	CB132570
33	1090.5	28.8	714	1	AJ396213
34	1080	28.5	942	3	B1599247
35	1075	28.3	666	1	AJ445231
36	1054	27.8	797	1	AJ454599
37	1041	27.4	761	6	CA317787
38	1040	27.4	765	5	BUS69071
39	1033	27.1	581	2	BP912750
40	1029.5	27.1	703	1	AJ441724
41	1018	26.8	717	7	CK365134
42	1011.5	26.7	1341	8	DN677970
43	1004.5	26.5	832	3	B1596814
44	1001.5	26.4	1264	10	AY415849
45	991	26.1	679	1	AM915532

#### ALIGNMENTS

RESULT 1  
LOCUS CR858790 2985 bp mRNA linear HTC 12-NOV-2004  
DEFINITION Pongo pygmaeus mRNA; CDNA DKFZp46811913 (from clone DKFZp46811913).  
ACCESSION CR858790  
VERSION CR858790.1 GI:55728505  
KEYWORDS HTC.  
SOURCE Pongo pygmaeus (orangutan)  
ORGANISM Pongo pygmaeus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Pongo.  
1 (bases 1 to 2985)  
Ottewaelder,B., Obermaier,B., Deutschenbauer,S., Schaipe,A.,  
Mewes,H.W., Well,B., Amid,C., Osanger,A., Fobo,G., Han,W. and  
Wiemann,S.  
The German CDNA Consortium  
Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764  
Neuherberg, GERMANY  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de/  
sequenced by Medigenomix (Martinried/Germany) within the CDNA  
sequencing consortium of the German Genome Project.  
This clone (DKFZp46811913) is available at the RZPD Deutsches  
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.  
Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp46811913  
Further information about the clone and the sequencing project is  
available at http://mips.gsf.de/projects/cdna/

REFERENCE  
AUTHORS  
CONSRMT  
TITLE  
JOURNAL  
COMMENT  
The German CDNA Consortium  
Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764  
Neuherberg, GERMANY  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de/  
sequenced by Medigenomix (Martinried/Germany) within the CDNA  
sequencing consortium of the German Genome Project.  
This clone (DKFZp46811913) is available at the RZPD Deutsches  
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.  
Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp46811913  
Further information about the clone and the sequencing project is  
available at http://mips.gsf.de/projects/cdna/

#### FEATURES

Location/Qualifiers

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ORIGIN

Alignment Scores:
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Best Local Similarity: 99.0% Mismatches: 5
Query Match: 99.1% Indels: 0
DB: 4 Gaps: 0

US-10-755-889-18 (1-706) x CR858790 (1-2985)

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Db 169 AACCTTAATGCTCTCCGAGTCGAGACATCTTGACTATGTTGATGTTGTGAGCGGT 228
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QY 61 PheThraPgiNeuLysCyAsnLeuSeRvAlIlEaSnLeuAaPProGluIlIeAnPro 80
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QY 221 AlaAnProPheProLyGluArGAlaLeuProCyAsaPSeRtAlaArGProVaLProLy 240
Db 769 GCCAACCCCTTCCCAAGAGCGGCGCTCCCATGTATGATGCGCAGCCAGTCTCTGT 828
QY 241 GluTySeRtArGProThrLeuGluVaLSeRProAnVaLcySHIsSeRtAnIlIeTySeR 260
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[illegible]

TITLE	JOURNAL	PUBMED	REFERENCE	AUTHORS
4	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium	Functional annotation of a full-length mouse cDNA collection	Nature 409, 685-690 (2001)	5
5	The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Nature 420, 563-573 (2002)	6 (bases 1 to 33107)
6	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hagiwara, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Kahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	Direct Submission	Submitted (16-JUL-2001) Yoshinhide Hayashizaki, The Institute of Physiological and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	7
7	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	Please visit our web site for further details.	URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers	8
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polya\_signal

/note="putative"

polya\_site

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ORIGIN

Alignment Scores:

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Percent Similarity:	96.2%	Conservative:	14
Best Local Similarity:	94.2%	Mismatches:	26
Query Match:	95.0%	Indels:	1
DB:	4	Gaps:	1

US-10-755-889-18 (1-706) x AK039228 (1-3307)

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Db	1971	CAGCTGCTCATCCACATCGAGAGAAAGCCGATACCCCTGTGTAAATCTGTGGACTCGCTTC	2030
QY	640	ArgHisLeuGlnInthrLeuIlySerHisLeuArgIleIshThnGlyIlyIleProIyThis	659
Db	2031	CGGACACCTTCAGACTTCGAGAGAGCCATCTCGCTCCACAAAGCCACGCACTTCATTGCGGCAG	2090
QY	660	CysGluIlySerCysAsnLeuHisPheArgHisIshIySerGlnLeuArgLeuHisLeuArgIln	679
Db	2091	TGTAGAAGAGGTAACTCGGACCTTCCTGCTACAAAGCCAAAGCCAGCACTTCATTGCGGCAG	2150
QY	680	IyshIshGlyAlaIleThrAsnThyIleValGlnIlyArgValSerAlaIshAspLeuPro	699
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QY	700	ProGluLeuProIyIyValaCys	706
Db	2211	CCGAGAGCTCCCAAGCCTGC	2231
RESULT 3			
LOCUS	AK036975	3289 bp	mRNA
DEFINITION	AK036975	Mus musculus adult female vagina cDNA, RIKEN full-length enriched library, clone:5930032A10 product:B-cell leukemia/lymphoma 6, full insert sequence.	
ACCESSION	AK036975		
VERSION	AK036975.1	GI:26331847	
KEYWORDS	AK036975	HTC	cap-trapper.
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	Carninci,P. and Hayashizaki,Y.		
JOURNAL	High-efficiency full-length cDNA cloning		
PUBMED	Meth. Enzymol. 303, 19-44 (1999)		
REFERENCE	10349636		
AUTHORS	2		
TITLE	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komo,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
PUBMED	Genome Res. 10 (10), 1617-1630 (2000)		
REFERENCE	11042159		
AUTHORS	3		
TITLE	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komo,H., Akiyama,J., Nishi,K., Kitsuina,T., Tashiro,H., Itoh,M., Suni,N., Ishi,Y., Nakamura,S., Hazama,N., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.		
JOURNAL	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multiplexillary sequencer		
PUBMED	Genome Res. 10 (11), 1757-1771 (2000)		
REFERENCE	11076861		
AUTHORS	4		
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.		
JOURNAL	Functional annotation of a full-length mouse cDNA collection		
PUBMED	Nature 409, 685-690 (2001)		
REFERENCE	5		
AUTHORS	The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
PUBMED	6 (bases 1 to 3289)		
REFERENCE	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,		

**TITLE**  
**JOURNAL**  
**COMMENT**  
**FEATURES**  
**source**  
**CDS**  
**ORIGIN**

Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 Hori F., Imoto K., Ishii Y., Itoh M., Kigawa I., Kasukawa T.,  
 Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M.,  
 Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M.,  
 Nakamura N., Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N.,  
 Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N.,  
 Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T.,  
 Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S.,  
 Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A.,  
 Muramatsu M. and Hayashizaki Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,  
 url: http://genome.gsc.riken.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)  
 CNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 url: http://genome.gsc.riken.jp/  
 url: http://fantom.gsc.riken.jp/.  
 Location/Qualifiers  
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US-10-755-889-18 (1-706) x AK036975 (1-3289)

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 Db 173 AACCTTAATGCTCTCGAGAGTGGAGACATCTTGACGAGAGCTGTGATCGTGGTACCGCT 232  
 Qy 41 GUGUlnPheArgIleAlaIleValThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle 60  
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ACCESSION	Genomic survey sequence.
VERSION	AY399831
KEYWORDS	AY399831.1 GI:39755820
SOURCE	GSS.
ORGANISM	Homo sapiens (human)
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TITLE	1 (bases 1 to 1977) Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tarenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios Science 302 (5652), 1960-1963 (2003)
JOURNAL	14671302
PUBMED	2 (bases 1 to 1977)
REFERENCE	Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tarenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
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QY	81 GluGluPheCysAlleLeuLeuAspPheMetYrThrSerArgLeuAsnLeuArgGluGly 100
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QY	121 CysArgLeuPheIleIysAlaSerGluValGluMetValSerAlaIleIysProProArg 140

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Db 1561 AATGATGTGATCTGCGCTTCTCTGAGAGGCTCTCACTAAGAGGACACGCTGACAGACC 1620

Qy 541 HisSerAaspLysProTyrLysCysAaspArgCysGluAlaSerPheArgTyrLysGluAen 560

Db 1621 CACAGTGACAAACCCCTACAAAGTGTGACCGCTGACAGGCTCTTCCGTACAAAGGGCAAC 1680

Qy 561 LeuAlaSerHisLysThrValHisThrGlyGluLysProTyrArgCysAenLysCysGly 580

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Db 1741 GCCCATTTCAACCGCCAGCCGACCTGAAACCCACACTCGAATTCACCTTGAGAGAGAG 1800

Qy 601 ProTyrLysCysGluThrCysGlyAlaArgPheValGlnValAlaHisLeuArgAlaHis 620

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Qy 621 ValLeuLysHisThrGlyGluLysProTyrProCysGluLysCysGlyThrArgPheArg 640

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Qy 641 HisLeuGlnThrLeuLysSerHisLeuArgGlyHisThrGlyGluLysProTyrHis 659

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RESULT 5  
LOCUS AY399833 1980 bp DNA linear GSS 15-DEC-2003  
DEFINITION Mus musculus BCL6 gene, VIRUTAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY399833  
VERSION AY399833.1 GI:39755822  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 1980)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
Adam, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1980)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
Adam, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source  
1..1980  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
<1..>1980  
/gene="BCL6"

ORIGIN  
/locus\_tag="HCM0355"  
US-10-755-889-18 (1-706) x AY399833 (1-1980)  
Alignment Scores: 3.04e-258 Length: 1980  
Pred. No.: 3351.50 Matches: 620  
Score: 96.14 Conservative: 15  
Percent Similarity: 96.14 Mismatches: 25  
Best Local Similarity: 93.94 Indels: 1  
Query Match: 88.44 Gaps: 1  
Db: 10  
1 MetAlaSerProAlaAaspSerCysIleGlnPheThrArgHisAlaSerAaspValLeuLeu 20  
1 ATGGCTCCCGGCTGACAGCTGTATCCAGTTTACCGGACGCTAGATGTTCTTCTCC 60  
21 AenLeuAenArgLeuArgSerArgAapIleLeuThrAaspValIleValValSerArg 40  
61 AACCTTAATCGCTCCGGAGTGGGACATCTTGAACGACGTTGTGATCGTGTGAGCCGT 120  
41 GlnGlnPheArgAlaHisLysThrValLeuMetAlaCysSerGlyLeuPheTyrSerIle 60  
121 GAGCAGTTTAAAGCCCATTAAGACAGTGTCTCAAGCTTGAAGCGGCTGTCTTACAGTATC 180  
61 PheThrAaspGlnLeuLysCysAenLeuSerValIleAenLeuAaspProGluIleAaspPro 80  
181 TTCATGACCACTTAATGCAACTTGTATGATCAATCTAATGATCTGAAATACAGCCCT 240  
81 GlnGlyPheCysIleLeuLeuAaspPheMetTyrThrSerArgLeuAenLeuArgGluGly 100  
241 GAGGGGTTTGGATCTCTCGTGAATTCATGTACATGACATGAGCTCAACCTGAGGAAAGCC 300  
101 AenIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGlnHisValValAapThr 120  
301 AATATCATGGCGGTATGACACACAGCTATGACCTGACAGATGAGACATGTGTGACACACA 360  
121 CysArgLysPheIleLysAlaSerGluAlaGluMetValSerAlaIleLysProProArg 140  
361 TCGAGGAATTCATCAAGCCGAGTACGAGCAAGAAATGCCCCCGCACTTAACTCCCGCT 420  
141 GlnGluPheLeuAenSerArgMetLeuMetProGlnAapIleMetAlaTyrArgGlyArg 160  
421 GAAAGTTCTTAACAGCGCGATGTGATGCCCATGACATGATGAGCTTACCGAAGTCTGT 480  
161 GluValValGluAenAenLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe 180  
481 GAGTCTGTGAGAAACATATGCACTGAGAAATACTCCCGGCTGTGAGAGCAAGCTTTT 540  
181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200  
541 GCTCTCTCTCTTCAAGTGGCTGTGACACACACACAGGCTCTTATCCCATGTACAGCCAT 600  
201 LeuProValSerSerLeuLeuPheSerAaspGluGluPheArgAaspVal---ArgMetPro 219  
601 CTCGGCTCAGACACCTTCTCTTCTGATGAGAGCTCCGAGATGCCCGCGAATGCTCT 660  
220 ValAlaAenProPhePheProLysGluArgAlaLeuProCysAaspSerAlaArgProValPro 239  
661 GTGGCCAAACCTTTTCCCAAGAGCGGTGCCCTCCCTGTGAAAGTGCACGAGCAAGTCCCT 720  
240 GlyGluTyrSerArgProThrLeuGluValAaspProAaspValCysHisSerAenLysTyr 259  
721 AATGATATTAAGACGCGCACCATTAAGAGTGTCTCCCAAGTTGTGTGTACAGCAATCTAC 780  
260 SerProLysGluThrIleProGluGluAlaArgSerAaspMetHisTyrSerValAlaGlu 279  
781 TCGCCCAAGAGAGAGTCCCAAGAGAGCTCGAAGTACATACATACATACATGAGTGTGAG 840  
280 GlyLeuLysProAlaAlaProSerAlaArgAenAlaProTyrPheProCysAaspLysAla 299  
841 GGCCCAAGCTGTGTCTCTTCTGTGCGAATGTCTCATACTTCCCTGTGACAAAGCC 900



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Db 301 ATGGCTGTATGGCCAGCGCTATGTACTGCAGATGAGCATGTTGTGACATTGCCCG 360
Qy 123 TyePheIleValLeuSerGluIaGluMetValSerAlaIleLysProPheArgGluIu 142
Db 361 AAGTTATTAAAGCCAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAG 420
Qy 143 PheLeuAspSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGluVal 162
Db 421 TTCCTTANACGCGCGATGCTGATGCTCCANNNNCATCATGGCCATATGGGGGTGTGAGGT 480
Qy 163 ValGluAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPheAlaPro 182
Db 481 GTGGAACAAACNNNTGCGNNNAGAGAGCGCCCTGGGTGTGAGAGAGAGCTTTGGCCCC 540
Qy 183 SerLeuTyrSerGlyLeuSerThrProPheAlaSerTyrSerMetTyrSerIleLeuPro 202
Db 541 AGCCTGTACAGTGGCTGTCCANNANCGCCAGCCNNNNATTCACATGACAGCCACCTCCCT 600
Qy 203 ValSerSerLeuLeuPheSerAspGluGluPheArgAspValArgMetProValAlaAsn 222
Db 601 GTGAGAGAGCTCTCTTCTCCGATGAGAGATTCCGGAGTCCGGATGCTGTGGCCAAAC 660
Qy 223 ProPheProGlyGluArgAlaLeuProCysAspSerAlaArgProValProGlyGluTyr 242
Db 661 CCTTCCCAAGAGCGGCACTCCCATGTGATGTCAGCCAGTCCCTGGTGAAGTAC 720
Qy 243 SerArgProThrLeuGluIuValSerProAsnValCysHisSerAsnIleTyrSerProLys 262
Db 721 AGCCGGCCGACTTGGAGGTGTCCTCCCAATGTGTGCACAGCAATATCTAATCAACCAAG 780
Qy 263 GluThrIleProGluGluIaIaArgSerAspMetHisTyrSerValAlaGluGlyLeuLys 282
Db 781 GAATACAGTCCCAAGAGGCAACAGATGATGCACTACAGTGTGGTGAGGCCCTCAAG 840
Qy 283 ProAlaIaIaProSerAlaIaArgAsnAlaProTyrPheProCysAspLysAlaSerGly 302
Db 841 CTGTGCTGCCCCCTCAGCCCAAAATGCCCCCTACTTCTGTGTGACAAAGCCACCAAGAA 900
Qy 303 GluGluAsnProSerSerGluAspGluIleAlaLeuHisPheGluProProAsnAlaPro 322
Db 901 GAAGAGAGACCTCTCTCGAAGATGATGATGCTCCATTTCAAGCCCCCAATGACACC 960
Qy 323 LeuAsnArgLysGlyLeuValSerProGlnSerProGlnLysSerAspCysGlnProAsn 342
Db 961 CTGAACCGGAAGGTCTGTGTTAGTCCACAGGCCCAAGAAATCTGATCTCCAGCCCAAC 1020
Qy 343 SerProThrGluIaIaCysSerSerLysAsnAlaCysIleLeuGlnAlaSerGlySerPro 362
Db 1021 TCGCCCAAGAGTCTGCAACAGATGATGATGCTGATCTCCAGAGCTTCTGGCTCCCT 1080
Qy 363 ProAlaLysSerProThrAspProLysAlaCysAsnTrpLysTyrLysPheIleVal 382
Db 1081 CCAAGCCAAAGACCCCACTGACCCCAAGCCCTGCAACTGGAAGAAATCAAGTTCACTGTG 1140
Qy 383 LeuAsnSerLeuAsnGlnAlaAsnAlaLysProGlyGlyProGluGlnAlaGluLeuGlyArg 402
Db 1141 CTCAACAGCTCTCAACCAAGATGCTCAACCAAGAGGAGCTTGAAGCTGAGGCGCC 1200
Qy 403 LeuSerProArgAlaTyrThrAlaProProAlaCysGlnProProMetGluProGluAsn 422
Db 1201 CTTTCCCAAGAGCTTCAACAGGCCCCCACTGCTGCGCAGCAACCATGAGAGCTGAAAC 1260
Qy 423 LeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIleProGln 442
Db 1261 CTGACCTTCAAGTCCCAACCAAGCTCAGGCGGAGGAGGACTCCACCATCCCAAA 1320
Qy 443 AlaserArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSerSerSer 462
Db 1321 GCCAGCGGCTCAATTAATCATGCTTAACAGGTCATGACGGGCTTCCCGCAGCAGCAGC 1380
Qy 463 GluSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySerGlnSer 482
Db 1381 GAGAGCCACATCACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440

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Qy 483 ProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGluMetGly 502
Db 1441 CCACAGCAGCAGCAGATGTGCTTCCACACCGCTGAGCCCAAGTCTCCAGAGAGATGGGA 1500
Qy 503 GluThrGlnSerGlyTyrSerAspSerCysGluAsnGlyAlaPhePheCysAsnGlu 522
Db 1501 GAGACCCAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Qy 523 CysAspCysArgPheSerGluGluIaIaSerLeuLysArgHisLeuGlnThrHisSer 542
Db 1561 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1620
Qy 543 AspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsnLeuAla 562
Db 1621 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1680
Qy 563 SerHisLysThrValHisThr 569
Db 1681 AGCCACAGACCGTCCATAC 1701

RESULT 7
BX431187
LOCUS
DEFINITION
BX431187 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS0DF021YF19 5-PRIME, mRNA sequence.
ACCESSION
BX431187
VERSION
BX431187.1 GI:30784988
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo
1 (bases 1 to 920)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 2184.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0BAP01E2C05_AF01476_1&c=2184.r

FEATURES
source
1..920
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF021YF19"
/cisue_type="FETAL BRAIN"
/dev_stage="Fetal"
/clone_1ib="Homo sapiens FETAL BRAIN"
/notes="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN
Alignment Scores:
Pred. No.: 2,19e-109 Length: 920
Score: 1493.00 Matches: 287
Percent Similarity: 94.1% Conservative: 2
Best Local Similarity: 93.5% Mismatches: 17
Query Match: 39.4% Indels: 2

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DB: 5 Gaps: 0

US-10-755-889-18 (1-706) x BX431187 (1-920)

QY 211 GluGluPheArgAPValArgMetProValAlaAsnProPheProGlyArgAlaLeu 230

DB 2 GAGGAGATTTCGGAATGTCGGAATGCTTGAGNCAACCTTCCAG-GAGCGGCACTC 60

QY 231 ProCysAspSerAlaArgProValProGlyValuTySerArgProThrLeuGluValSer 250

DB 61 CCAATGATGATGCGCAGCGGCAAGTCCCTGGAGAGACCGCGGCACTTTGGAGGTGTC 120

QY 251 ProAsnValCysHisSerAsnLeuTySerProGlySerGluThrLeuProGluGluAlaArg 270

DB 121 CCCAATGTGTGCCACGCAATATCTATTCACCCAGAGAACATCCAGAGAGGCGACGA 180

QY 271 SerAspMetHisTySerValAlaGluGlyLeuValProAlaAlaProSerAlaArgAsn 290

DB 181 AGTGAATATGCACTACAGATGTGGCTGAGAGGCTCAAACTGTGCTGCTCCCTCAGCCGAAAT 240

QY 291 AlaProTyRPhProCysAspLysAlaSerLysGluGluGluArgProSerSerGluAsp 310

DB 241 GCCCTCACTTCCCTTGTGACAGGCGCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAT 300

QY 311 GluIleAlaLeuHisPheGluProProAsnAlaProLeuAsnArgLysGlyLeuValSer 330

DB 301 GAGATTCCTGCAATTCGAGCCGCCCAATGCACTCCCTGAAACCGAGGCTGTGTTAGT 360

QY 331 ProGluSerProGluLysSerAspCysGluProAsnSerProThrGluAlaCysSerSer 350

DB 361 CCACAGAGCGCCCGAATCTGACTGCGCAGCCCAACTGCGCCACAGAGCTCTGACAGAGT 420

QY 351 LysAsnAlaCysIleLeuGlnAlaSerGlySerProProAlaLysSerProThrAspPro 370

DB 421 AAGATATCTGATCTCTCCAGGCTTGTGCTCCCTCCAGCAGAGAGAGAGAGAGAGAG 480

QY 371 LysAlaCysAsnTrpLysLysTyLysPheIleValLeuAsnSerLeuAsnGlnAsnAla 390

DB 481 AAGACCTGCACTGGAAGAAATACAGTTCATGCTGCTCAACAGCCTCAATCAGAAATGCC 540

QY 391 LysProGluGlyProGluGlnAlaGluLeuGlyArgLeuSerProArgAlaTyThrAla 410

DB 541 AAACCAAGAGGCGCTGAGCAGGCTGAGCTGAGCGCTTCTCCACAGAGCTTACACGAGNC 600

QY 411 ProProAlaCysGlnProProMetGluProGluAsnLeuAspLeuGlnSerProThrLys 430

DB 601 NCACCTGCTGCGCAGCCAGCCATGAGCTTGAACCTTGACCTCCAGTCCCAACAG 660

QY 431 LeuSerAlaSer-GlyLysAspSerThrIleProGlnAlaSerArgLeuAsnAlaIleVal 450

DB 661 CTGATGCGCAGCGGAGGAGAGACTCCACATCCCAAGAGCGGCTCATTAACATCGT 720

QY 450 LAsnArgSerMetThrGlySerProArgSerSerSerGluSerIleSerProLeuTyRMe 470

DB 721 TTAACAGGTTCATGACGGCTCTCCCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 780

QY 470 HisProProLysCysThrSerCysGlySerGlnSerProGlnHisAlaGluMetCysLe 490

DB 781 GCACCCCGCAGAGTGCAGCTTCTGAGTTCAGTCCACAGCATGACAGAGAGATGCTCT 840

QY 490 uHisThrAlaGlyProThrPheAlaGluGluMetGlyLysThrGlnSerGluTyRSerAs 510

DB 841 TCACACCGTGGGCGCAGCTTCCCTTGGAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAT 900

QY 510 pSerSerCysGluLysGly 516

DB 901 TTCTAGCTGGAGAGAGCGG 919

RESULT 8

CX565176 859 bp mRNA linear EST 12-JAN-2005

LOCUS CX565176

DEFINITION UT-M-HA0-cuj-f-01-0-UT.r1 NIH\_BMAP\_HA0 Mus musculus cDNA clone

IMAGE:6735458 5', mRNA sequence.

ACCESSION CX565176

VERSION CX565176.1 GI:57592205

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 859)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgabbs-rc@mail.nih.gov](mailto:cgabbs-rc@mail.nih.gov)

Tissue Procurement: Dr. James Lin University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mouse1.html>

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1. 859

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6"

/db\_xref="taxon:10090"

/clone="IMAGE:6735458"

/tissue\_type="whole eye"

/dev\_stage="embryo 12.5,13.5,14.5 dpc"

/lab\_host="DH10B (11 phage resistant)"

/clone\_1ib="NIH BMAP HA0"

/note="Organ: Eye; Vector: pYX-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according to Bontade, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTAATGAAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 1,18e-105 Length: 859

Score: 1446.00 Matches: 266

Percent Similarity: 95.4% Conservative: 3

Best Local Similarity: 94.3% Mismatches: 13

Query Match: 38.1% Indels: 0

DB: 8 Gaps: 0

US-10-755-889-18 (1-706) x CX565176 (1-859)

QY 277 ValAlaGluGlyLeuLysProAlaAlaProSerAlaArgAsnAlaProTyRPhProCys 296

DB 14 GTGCTGAGGCGCCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 73

QY 297 AspLysAlaSerLysGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPhe 316

DB 74 GACAAAGCCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGCT 133

QY 317 GluProProAsnAlaProLeuAsnArgLysGlyLeuValSerProGlnSerProGlnLys 336

DB 134 GAGCCCGCCCAATGACCTTGAACCGGAGAGGTGTGTTAGTCCCGAGAGTCCCGCAGAA 193



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Qy 337 SerAspCysGlnProAsnSerProThrGlnAlaCysSerSerIysAsnAlaCysIleLeu 356
Db 194 TCCGACCTGCGCCCAACTCACCACAGAGTCTTCGACGACGAGAACCGCTTCATCTT 253
Qy 357 GlnAlaSerGlySerProProAlaIlySerProThrAspProIlysaIaCysAsnTrpLys 376
Db 254 CAGGCGCTGCTGCTCCGCGCAGCAGAACGCCCACTGACCCGGAAGCCTGCACTGGAAG 313
Qy 377 LysTrpLysPheIleValIleuAsnSerLeuAsnGlnAlaIlySerProGlyGlyProGlu 396
Db 314 AACCTAAAGATTCAATCGTTCTCAACAGCTTCATCAAGAAAGTCCAAACCCGAGGCTCTGAG 373
Qy 397 GlnAlaGluLeuGlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnPro 416
Db 374 CAGGCAAGCTGGAGTGGCTCTCTCCCTCGAGCTTACCTGACCGCCGCTTCCAGCCG 433
Qy 417 ProMetGluProGluIleuAsnLeuAsnLeuGlnSerProThrLysLeuSerAlaSerGlyGlu 436
Db 434 CTTATGAGCCCGGAACTTGTATCTTCAGTCCCGCAGGCTCAAGTCCAGTGGGGAG 493
Qy 437 ArgSerThrIleProGlnAlaSerArgLeuAsnAlaIleValAsnArgSerMetThrGly 456
Db 494 GACTTACCACTCCCGCAGCAGCCGCTCAATATCTCGTGAACAGTCCCTGCGAGAGC 553
Qy 457 SerProArgSerSerSerArgIlySerIlySerProLeuTyrMetIlySerProIlyCysTrp 476
Db 554 TCCCGCCGAGCAGAGTGAAGTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 613
Qy 477 SerCysGlySerGlnSerProGlnAlaIleGluMetCysLeuIlyThrAlaGlyProThr 496
Db 614 TCCGCGGCTCTCAGTCCCGCAGCAGATACAGAGATGCTCCATACACTGCTGGGCCAGC 673
Qy 497 PheAlaGluLeuMetGlyGlyThrGlnSerGlyTyrSerAspSerSerCysGluAsnGly 516
Db 674 TTCGCGGAGAGATGGGGAAACCCAGTCAAGATTCGGAATTCAGCTGTGGAATGG 733
Qy 517 AlaPhePheCysAsnGluCysAspCysArgPheSerGlnGlnAlaSerLeuLysArgHis 536
Db 734 ACCTTCTTTCGCAACGATGAGTCTGCTTCTCTGAGAGGCTCTGCTCAAGAGGAC 793
Qy 537 ThrLeuGlnThrIlySerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArg 556
Db 794 ACCTGCAAGACGACAGTGACTAATCATATGATGATCTGCGCAGGCTCTCTTCGCG 853
Qy 557 TyrLys 558
Db 854 TACAAG 859

RESULT 9
LOCUS BMS50970 1092 bp mRNA linear EST 20-FEB-2002
DEFINITION AGNCOURT_6544992 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5738450
5', mRNA sequence.
ACCESSION BMS50970
VERSION BMS50970.1 GI:18787602
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 1092)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@bms-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:

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http://image.lnl.gov
Plate: LLM12750 row: d column: 03
High quality sequence stop: 635.
FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5738450"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_11b="NIH_MGC_88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: NciI; Site 2: SalI; Cloned unidirectionally;
oligo-dt primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: This is a NIH_MGC Library."

ORIGIN
Alignment Scores:
pred. No.: 1,976-101 Length: 1092
Score: 1395.50 Matches: 293
Percent Similarity: 89.74 Conservative: 12
Best Local Similarity: 86.24 Mismatches: 24
Query Match: 36.84 Indels: 11
DB: 3 Gaps: 4

US-10-755-889-18 (1-706) x BMS50970 (1-1092)
Qy 1 MetAlaSerProAlaAspSerCysIleGlnPheThrArgHisAlaSerAspValLeuLeu 20
Db 75 ATGGCTCCGCGGCTGACAGCTGTATCCAGTTCACCCGCGCAGTCAAGTATGTTCTTCTC 134
Qy 21 AsnLeuAsnArgLeuAsnSerArgAspIleLeuThrAspValIleValIleSerArg 40
Db 135 AACCTTAATCGTCTCGGAGTCAAGATCTGAGTCAAGTGTGATGTTGTGAGCCGT 194
Qy 41 GlnGlnPheArgAlaHisIlyThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle 60
Db 195 GAGCAGTTTAGAGCCCATTAAGCGTCTCTCAAGGCTGAGAGGCTGCTCTCTATAGATC 254
Qy 61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
Db 255 TTTACAGACAGATTGAATGCAACCTAGTATGATCAATCTAGATCTGATCAACCTCT 314
Qy 81 GlnGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100
Db 315 GAGGATTCGTGATCTCTCTGAGCTTCATGATCAATCTCGGCTCAATTCGAGAGGCG 374
Qy 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValIleAspThr 120
Db 375 AACATATGCTGTATGATGCGCAGGCTATGCTACATGAGATGAGATGTTGTGAGCAT 434
Qy 121 CysArgLysPheIleValIleuAsnSerGlnAlaGluMetValSerAlaIleLysProArg 140
Db 435 TGCCGAGATTATTAAGCCAGTGAAGCAGATGTTTCTGCCATCAAGCTCTCTCGT 494
Qy 141 GlnGlnPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160
Db 495 GAAGAGTTCCTCAACGCGCGAGTGCATGATGCCCAAGATATGAGCTATCGGGTCTGT 554
Qy 161 GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe 180
Db 555 GAGGTGTGAGAACCACTGCTCAGAGAGAGGCGCCCTGGGTGTAGAGCAGAGCCCTT 614
Qy 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
Db 615 GCCCGAGCTGTACAGTGGCTGTGACACCGCGCCTTATTCATGTACAGCCAC 674
Qy 201 LeuProValSerSerLeuLeuPheSerArgGluGlnPheArgAspValIlyMetProVal 220
Db 675 CTCCTGTGAGCAGCTCTCTCTTCTCGATGAGAGATTTCCGAGATGCTCGAGTCTGTG 734

```



QY 221 AlaAsnProPheProlysgluArgAlaLeuProCysAspSerAlaArgProValProGly 240  
 DB 735 GCCAAACCTTCCCGGAGCGGCACTCCCAATGATAGTGCAGGCGACCTCTGT 794  
 QY 241 GltTysSerArgProThr-LeuGluValSer-ProAsnValCysHisSerAsnIleTyrS 260  
 DB 795 GAGTACGCGCGGCACTTTTGAGGTCTCCCGCAAGGGGTGCACAGCATATCTATT 854  
 QY 260 exProlysgluThrIleProGluGluAlaArgSerAspMetHisTyrSerValAla---G 279  
 DB 855 CCCCAGGAAGAACATTCCTCCAAAGAGGCAACCAATGATATGCTTCACGGGCGCTGA 914  
 QY 279 luGluLeuValProAla--AlaProSerAlaArgAsnAla-ProTyrPheProCysAsp 298  
 DB 915 GGGGCTCCCAACCTGTGCTGCTCCCAACCGAAAGCCCTCTACTCTCCCTTGAGCA 974  
 QY 298 ysAla-SerlysgluGluArg-----ProSerSerGluAspGluIleAlaLeuHis 315  
 DB 975 AGGCCCCCAAGAAAGAAAGAAAGAACCTCTCTCCGAAAGAAATTAATGCTTGAT 1034  
 QY 316 PheGluProProAsn---AlaProLeuAsn---ArglysglyLeuVal 329  
 DB 1035 TTTCAAGGCCCCCAATGGGCCCCCTTAACCCGAAAGGCTCTGTG 1082  
 RESULT 10  
 BQ722826 856 bp mRNA linear EST 16-JUL-2002  
 LOCUS AGENCOURT 8241329 Lupski sympathetic\_trunk Homo sapiens cDNA clone  
 DEFINITION IMAGE:6187194.5', mRNA sequence.  
 ACCESSION BQ722826 GI:21861723  
 VERSION BQ722826.1 GI:21861723  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 856)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LMNL at:  
 http://image.llnl.gov  
 Plate: LAM13580 row: m column: 19  
 High quality sequence stop: 637.  
 Location/Qualifiers  
 1..856  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6187194"  
 /sex="male"  
 /tissue\_type="sympathetic trunk"  
 /dev\_stage="adult, 16 yr"  
 /lab\_host="DH10B"  
 /clone\_lib="Lupski sympathetic trunk"  
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:  
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.  
 Directionally cloned using the following adaptors:  
 5'-TCGACCAAGCGCTCG-3' and  
 5'-GACTAGTCTAGATCGGCGCGCCCT(15)-3'. Size selected >  
 1 kb for average insert length 1.9 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine); available through Life  
 technologies."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1,79e-100 Length: 856  
 Score: 1381.50 Matches: 274  
 Percent Similarity: 97.9% Conservative: 3  
 Best Local Similarity: 96.8% Mismatches: 1  
 Query Match: 36.4% Indels: 5  
 DB: 5 Gaps: 1  
 US-10-755-889-18 (1-706) x BQ722826 (1-856)  
 QY 60 IlePheThrAspGluLeuValCysAsnLeuSerValIleAsnLeuAspProGluIleAsn 79  
 DB 3 ATCTTACAGACCAAGTTGAATGCAACCTTAGTGTATGATCATATCTAGATCTGATCAAC 62  
 QY 80 ProGluGluPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuValGlu 99  
 DB 63 CCGAGGAGATTCTGCACTCTCTGACTTATGATCATATCTGCGCTCAATTTGCGGAG 122  
 QY 100 GlyAsnIleMetAlaValMetAlaThrAlaMetTyrLeuGluMetGluHisValAsp 119  
 DB 123 GGCACACATCATGTGCTGTGATGGCCAGCGCTATGACTGACAGATGGATGTTGTGAC 182  
 QY 120 ThrCysArglyspPheIleValAlaSerGluAlaGluMetValSerAlaIleValProPro 139  
 DB 183 ACTTCCGGAAGTTTATTAGGCCAGTGAAGCAAGATGTTTCTGCCATCAAGCTTCT 242  
 QY 140 ArgGluGluPheLeuAsnSerArgMetLeuMetProGluAspIleMetAlaTyrArgGly 159  
 DB 243 CGTGAAGAGTTCTCAACAGCCGAGATGCTATGCTCCCAAGACATCATGCGGAGGT 302  
 QY 160 ArgGluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAla 179  
 DB 303 CGTGAAGGTGTGGAGAACCACTGCACTGAGAGCCCTGGGTGTGAGAGCAGAGCC 362  
 QY 180 PheAlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSer 199  
 DB 363 TTTGCCCCCAGCTGTAGAGTGGCTGTCCACAGCCGACCTTTTTCATATACAGC 422  
 QY 200 HisLeuProValSerSerLeuLeuPheSerAspGluPheArgAspValArgMetPro 219  
 DB 423 CACTCTCTGTACAGACCTCTCTTCTCCGATGAGAGTTTGGGATGTCGATGCT 482  
 QY 220 ValAlaAsnProPheProlysgluArgAlaLeuProCysAspSerAlaArgProValPro 239  
 DB 483 GTGGCCAAACCTTCCCGGAGCGGCACTCCATGATAGTGCAGGCCAGTCTCT 542  
 QY 240 GltTysSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyrS 259  
 DB 543 GGTAGTACAGCCCGCGCACTTGGAGGTGTCCCAATGTGTCCACAGCAATATCTAT 602  
 QY 260 SerProlysgluThrIleProGluGluAlaArgSerAspMetHisTyr-SerValAlaG 279  
 DB 603 TCACCAAGGAAGAACATTCCTCCAAAGAGGCAACGATATGACTCCCAATGTGGCTGA 662  
 QY 279 uGlyLeuValProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspVal 299  
 DB 663 GGGCTCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722  
 QY 299 aserlysgluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProP 319  
 DB 723 CAGCAAGGAAGAAAGAGACCTCTCTGGAAGATGAGATGCTGCAATTCAGAGCCCC 782  
 QY 319 asnAlaProLeu--AsnArglyGlyLeu-ValSerPro---GlnSerProGlnTyrS 337  
 DB 783 CAATGACCTCTGGAACCGAAAGAGTGTGGTTATGTTCCACAGAGCCCGAGAAATC 842  
 QY 337 T 337  
 DB 843 T 843  
 RESULT 11

BM801045  
 LOCUS BM801045 1004 bp mRNA linear EST 05-MAR-2002  
 DEFINITION AGENCOURT\_6422527 NIH\_MGC\_92 Homo sapiens cDNA clone IMAGE:5586337  
 5', mRNA sequence.  
 ACCESSION BM801045  
 VERSION BM801045.1 GI:19117868  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 1 (bases 1 to 1004)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [gsb@bbs-rcmail.nih.gov](mailto:gsb@bbs-rcmail.nih.gov)  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
 Plate: LHAM2354 row: b column: 02  
 High quality sequence stop: 608.  
 Location/Qualifiers

## FEATURES

## source

1. 1004  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5586337"  
 /cissue\_type="embryonal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_id="NIH\_MGC\_92"  
 /note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 2.5 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 8.5e-99 Length: 1004  
 Score: 1362.00 Matches: 279  
 Percent Similarity: 87.9% Conservative: 4  
 Best Local Similarity: 86.6% Mismatches: 10  
 Query Match: 35.9% Indels: 29  
 DB: 3 Gaps: 3

US-10-755-889-18 (1-706) x BM801045 (1-1004)

QY 160 ArgGluValAlaGluAsnAnuLeuProLeuArgSerAlaProGlyCysGluSerArgAla 179  
 Db 1 CGTGAAGTGTGGAGAACAACTGCACTAGAGAGCGCCCTGGTGTGAGAGAGAGCC 60  
 QY 180 PheAlaProSerLeuTyYSerGlyLeuSerThrProProAlaSerTyYSerMetTyYSer 199  
 Db 61 TTGGCCCCCAGCCGTGACGTGGCTGTCCACACCGCAGCCTTATTCATGTACAGC 120  
 QY 200 HisLeuProValSerSerLeuLeuPheSerPheSerGluGluPheArgPheValArgMetPro 219  
 Db 121 CACTCCCTCGACACACCTCTCTCTCCGAGAGAGATTTCGGAGTGTCCGGATCCCT 180  
 QY 220 ValAlaAsnProPheProTyYSGluArgAlaLeuProCysAspSerAlaArgProValPro 239  
 Db 181 GTGGCCAAACCTTCCCAAGAGAGCGGCACTCCCATGTATGTGCGACGCAAGTCCCT 240  
 QY 240 GlyGluTyYSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyY 259  
 Db 241 GGTGATGACAGCCGCGGCACTTTGGAGGTGTCCCAATGTGTGCGCACAGCAATATCTAT 300

QY 260 SerProTyYSGluThrIleProGluValArgSerAspMetHisTyYSerValAlaGlu 279  
 Db 301 TCACCCAGAGAAACATCCACAGAGAGCGACGAACTGATATGCACTACAGTGTGCTGAG 360  
 QY 280 GlyLeuTyYProAlaAlaProSerAlaArgAsnAlaProTyYProPheProCysAspTyYAla 299  
 Db 361 GGCCTCAACCTGCTGCGCCCTCCACGCCGAAATGTGCTACTCTCTTGTGACAGGCG 420  
 QY 300 SerTyYSGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProPro 319  
 Db 421 ACCAAGAGAGAGAGAGACCTCTCTCGAAGATGATGCTCCGCTGATTTGAGGCCCCC 480  
 QY 320 AsnAlaProLeuAsnArgGlyGlyLeuValSerProGlnSerProGlnTyYSerAspCys 339  
 Db 481 AATGACACCTGTAACCGAGAGGTCTGGTTAGTCCACAGAGCCCCCAGAAATCTGATGCG 540  
 QY 340 GlnProAsnSerProThrGluAlaCysSerSerTyYAsnAlaCysIleLeuGlnAlaSer 359  
 Db 541 CAGCCCACTCCGCCACAGAGCTGACAGCACTGAAGAAATGCTTCATCTCCAGGCTCT 600  
 QY 360 GlySerProProAlaValSerProThrAspProTyYAlaCysAsnTyYSerTyYIle 379  
 Db 601 GGCTCCCTCCAGCCAGAGGCCCACTGACCCCAAGGCTGCACTGGAGAAATACAG 660  
 QY 380 PheIleValLeuAsnSerLeuAsnGlnAsnAlaTyYPro-GlyGlyProGluGlnAla-G 399  
 Db 661 TTCATCTGTCTCAACAGCTCATCAGATGCAACCAAGAGAGGCGCTGACAGGCGCTG 720  
 QY 399 IuLeuGlyArgLeuSerProArgAlaTyYThr-AlaProProAla-CysGlnProPro 418  
 Db 721 ACTGGGCGCGCTTTTCCACAGGCTACACGCGGCCCTGCTGCTGACAGCCCAT 780  
 QY 418 rGluProGlu-AsnLeu-AspLeuGlnSerProThr-LysLeuSer-----AlaSerG 435  
 Db 781 GAGGCCGAGAAACCTTGACCTCCAGTCCCAAGCTTGGAAGTCCCGCGCGGAG 840  
 QY 435 yGluAspSerThrIleProGlnAlaSerArgLeuAsnIleValAsnArgSerMetTh 455  
 Db 841 AGGACTTCCCATTTCC----- 859  
 QY 455 rGlySerProArgSerSerSerGluSerHisSerProLeuTyYMetHisPro 472  
 Db 860 -----CCCAAGCCAGCCCGGAGTACATATA-----CATCCC 892

## RESULT 12

AJ454603/C AJ454603 800 bp mRNA linear EST 22-APR-2002

LOCUS AJ454603 riken1 Gallus gallus cDNA clone 3d2082, mRNA sequence.

DEFINITION AJ454603

ACCESSION AJ454603

VERSION AJ454603.1 GI:20264699

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

REFERENCE Buerstedde, J.M.

AUTHORS Buerstedde, J.M.

TITLE Gallus gallus bursa lymphocyte EST

JOURNAL Unpublished (2002)

CONTACT: Buerstedde JM

CELLULAR IMMUNOLOGY

HEINRICH-PETTE-INSTITUTE

MARTINSTR. 52, 20251 HAMBURG, GERMANY

EMAIL: <http://genetics.hpi.uni-hamburg.de/dt40est.html>.

## FEATURES

1. 800

Location/Qualifiers

/organism="Gallus gallus"

/mol\_type="mRNA"

/db\_xref="taxon:9031"

/clone="3d2082"

/cell\_type="bursal lymphocyte"

/dev\_stage="2-3 weeks old"

ORIGIN  
/clone 11b="r1ken1"  
/note="CB indred strain"

## Alignment Scores:

Pred. No.:	8.82e-97	Length:	800
Score:	1335.00	Matches:	241
Percent Similarity:	93.6%	Conservative:	8
Best Local Similarity:	90.6%	Mismatches:	17
Query Match:	35.2%	Indels:	0
DB:	1	Gaps:	0

US-10-755-889-18 (1-706) x AJ454603 (1-800)

```
QY 438 SerThrIleProGlnAlaSerArgLeuAsnIleValAsnArgSerMetThrGlySer 457
    |||||
DB 798 TCCAAATATCCCGCAAGGAGAGAGACTCAACAACATTGTAAACAGTCCNGGAGATGGCTCC 739

QY 458 ProArgSerSerSerGlySerHisSerProLeuThrMetHisProProGlySerThrSer 477
    |||||
DB 738 CCGGCGCAA-GCAAGTGAAGGAGGAGGAGTCCCGCTTACATGATTCATGAAAGTGCAGCTCC 680

QY 478 CysGlySerGlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPhe 497
    |||||
DB 679 TGGGATGCCAGTCCCGCAACATGATGATGCTTCAACCTCTGGCTCAGCTTT 620

QY 498 AlaGluGluMetGlyGluThrGlnSerGlySerAspSerSerCysGluAsnGlyAla 517
    |||||
DB 619 GGAAGAAAGATGGGGGAAACCCAGTCTGAGTACTGACTCAGNTGGGAGAACGAGCC 560

QY 518 PhePheCysAsnGluCysAspCysArgPheSerGluGluAlaSerLeuValArgHisThr 537
    |||||
DB 559 TTCTTCTGCAACGAGTGTGACTGCCGGTTCTCCAGAGGAGGCTCGCTCAAGAGGACACTCT 500

QY 538 LeuGlnThrHisSerAspLeuProGlyTrpCysAspArgCysGlnAlaSerPheArgTrp 557
    |||||
DB 499 CTGCAAGTCCACACGCAAAACCTTACAGTGCACGCTCCAGGCTCTTCCGCTTAC 440

QY 558 LysGlyAsnLeuAlaSerHisAluThrValHisThrGlyGlyLeuProGlyArgCysAsn 577
    |||||
DB 439 AAGGGGAACCTCGGCAAGCACAACACCTCCACAGAGAGAAAGCCGTCACGCTGCAC 380

QY 578 IleCysGlyAlaGlnPheAsnArgProAlaAsnLeuValHisThrHisThrArgHisSer 597
    |||||
DB 379 ATCTGTGGGGGCGAGTTCACCGGCGCAGCCCAACCTGAAACCCACACACGTAATTCACCTCC 320

QY 598 GlyGlyLeuProGlyTrpCysGlyLeuThrCysGlyAlaArgPheValGlnValHisSer 617
    |||||
DB 319 GGAAGAAAGATGGGGGAAACCCAGTCTGAGTACTGACTCAGNTGGGAGAACGAGCC 260

QY 618 ArgAlaHisValLeuIleHisThrGlyGlyLeuProGlyArgCysGlyThr 637
    |||||
DB 259 CGTGTCTATGTCTCATTCATCTGAGGAGAGAACCATCCCTGAGATCTGTGSCACA 200

QY 638 ArgPheArgHisAluGlnThrLeuValSerHisLeuArgHisThrGlyGlyLeuPro 657
    |||||
DB 199 CGTTTCCGCGACCTGCAACCTCAAAAGCCACTTGAATTCACACAGCGGCGAGAAACCT 140

QY 658 TyrHisCysGlyLeuValCysAsnLeuHisPheArgHisValSerGlnLeuArgLeuHisSer 677
    |||||
DB 139 TATCATTTGTGAAGATGCACTGCACTTCGCGCAAAAGCCAGCATCGGCTGCACTG 80

QY 678 ArgGlnLysHisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAsp 697
    |||||
DB 79 CGGCAAGAAAGACGGGGCCATCAACAACAGAGTGCATCCGATCTCGGCGCAACGAG 20

QY 698 LeuProProGluLeuPro 703
    |||||
DB 19 GTGCTCCGAGACTCCCC 2

LOCUS B0716058 804 bp mRNA linear EST 16-JUL-2002
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DEFINITION  
AGENCOURT 8103534 lupski sympathetic\_trunk Homo sapiens cDNA clone  
IMAGE:6190896 5', mRNA sequence.

ACCESSION  
B0716058

VERSION  
B0716058.1 GI:21854955

KEYWORDS  
EST.

SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens

REFERENCE  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

AUTHORS  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

TITLE  
Tissue Procurement: Dr. James R. Lupski  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LIML at:  
<http://image.llnl.gov>  
Plate: LHAM3590 row: h column: 01  
High quality sequence stop: 688.

FEATURES  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6190896"  
/sex="male"  
/tissue\_type="sympathetic trunk"  
/dev\_stage="adult, 16 yr"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
/note="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
NOTI; Site 2: SalI; cDNA made by oligo-dT priming.  
Directionally cloned using the following adaptors:  
5'-TCGACCCAGCGGTCG-3' and  
5'-GACTAGTTCATGATCCGAGCGGCGGCTT(15)-3'. Size selected >  
1 kb for average insert length 1.9 kb. This is a primary  
library, non-amplified. Library constructed by Life  
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
College of Medicine); available through Life  
Technologies."

## ORIGIN

## Alignment Scores:

Pred. No.:	1.7e-96	Length:	804
Score:	1331.50	Matches:	260
Percent Similarity:	97.4%	Conservative:	0
Best Local Similarity:	97.4%	Mismatches:	6
Query Match:	35.1%	Indels:	1
DB:	5	Gaps:	1

US-10-755-889-18 (1-706) x B0716058 (1-804)

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QY 21 AsnLeuAsnArgLeuAspSerArgAspIleLeuThrAspValValIleValSerArg 40
    |||||
DB 3 AACCTTAATGCTCTCCGAGTCCAGACATCTGATCTATGTGTGATGAGCGCT 62

QY 41 GluGlnPheArgAlaHisValThrValLeuMetAlaCysSerGlyLeuPheTyrSerIle 60
    |||||
DB 63 GAGCAGTTTAGAGCCCAATAAAACGCTCTCATGCGCTGCAAGTGCCTGTTCTATAGCATC 122

QY 61 PheThrArgGlnLeuValCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
    |||||
DB 123 TTTCAGACCAAGTGAATGCACTTGAAGTGTATGATCTGAGATCAACCTT 182

QY 81 GluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100
    |||||
DB 183 GAGGATTTCTGATCTCTGACTTCATGTACATCTCGGCTCAATTTGGGAGAGGC 242
```

QY 101 AenlleMeAlaValMeAlaThraAlaMeTyrLeuGluMeGluHisValAlaAspThr 120  
 Db 243 AACATATGAGCTGTGTATGGCAAGGCTATGTACTTCAATGAGATGTTGGACACT 302  
 QY 121 CysArgLysPheIleValAspSerGluAlaGluMetValSerAlaIleLysProProArg 140  
 Db 303 TGGCGGAAGTTTATTAAAGCGAGTGAAGAGATGTTTCTGCCATCAAGCTCTCGT 362  
 QY 141 GluGluPheLeuAsnSerArgMetLeuMetProGlnAspIleMeAlaTyrArgGlyArg 160  
 Db 363 GAAGAGTTCTCAACAGCCGAGTGTGATGCCCAAGACATCATGTCCATCGGGTCTGT 422  
 QY 161 GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe 180  
 Db 423 GAAGTGTGAGAAACAACCTGCACTGAGAGAGCCCTGGTGGTGAAGACAGAGCTTT 482  
 QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200  
 Db 483 GCGCCAGAGCTGTACAGTGGCTGTGTCAACAGCCGACCTTTATTCATGTACAGCCAG 542  
 QY 201 LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspValArgMetProVal 220  
 Db 543 CTCCTGTGACAGAGCTCTCTCTCCGATGAGAGATTTCCGGATGTCCGGATGCCGTGT 602  
 QY 221 AlaAsnProPheProLysGluArgAlaLeuProCysAsnSerAlaArgProValProGly 240  
 Db 603 GCCAACCCCTTCCCAAGAGGAGGAGGAGCTCCCATGTATGTCCAGGCGACATCCCTGT 662  
 QY 241 GluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyrSer 260  
 Db 663 GAGTACAGCCGGCGAGCTTTGAGAGTGTCCCAATGTGTGCCCGACATATCTATTCA 722  
 QY 261 ProLysGluThrIleProGluGluAlaArgSerAspMetHisTyrSerValAla---Glu 279  
 Db 723 CCCAAGAAACAATCCCAAGAGGAGGAGCATGATATGATGATGATGATGATGATGATG 782  
 QY 280 GlyLeuLysProAlaAlaPro 286  
 Db 783 GCCCTCAACCTCTGCTGCCCC 803

RESULT 14  
 LOCUS BX419860 849 bp mRNA linear EST 01-MAY-2004  
 DEFINITION BX419860 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
 CS0DF021YF19 5-PRIME, mRNA sequence.  
 ACCESSION BX419860  
 VERSION BX419860.2 GI:46925086  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 849)  
 J.M.B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On May 13, 2003 this sequence version replaced gi:30638052.  
 COMMENT  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE  
 Email: beqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
 was not normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.  
 This sequence belongs to sequence cluster 2184.r  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?ns=CS0DF021CC10CP1&c=2184.r.

FEATURES  
 source

Location/Qualifiers  
 1..849

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DF021YF19"  
 /libase\_type="FETAL BRAIN"  
 /dev\_stage="fetal"  
 /clone\_lib="Homo sapiens FETAL BRAIN"  
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-strand cDNA was digested with Not I and  
 EcoRV sites of the pCMVSPORT 6  
 vector. Library was not normalized."

# ORIGIN

Alignment Scores:  
 Pred. No.: 8,4e-93 Length: 849  
 Score: 1286.00 Matches: 250  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 33.9% Indels: 0  
 DB: 5 Gaps: 0

US-10-755-889-18 (1-706) x BX419860 (1-849)

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 Db 220 GAGCAGTTTAGAGCCCATTAACGGTCTTCATAGGCTGCAGAGGCTGTCTTATAGCATC 279  
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ACCESSION AJ441866  
VERSION AJ441866.1 GI:20209087  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Bukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 798)  
Buerstedde, J.M.  
REFERENCE Buerstedde, J.M.  
AUTHORS Gallus gallus bursal lymphocyte EST  
TITLE Unpublished (2002)  
JOURNAL Contact: Buerstedde JM  
COMMENT Cellular Immunology  
Heinrich-Pette-Institute  
Martinistr. 52, 20251 Hamburg, Germany  
Email: URL: <http://genetics.mpi.uni-hamburg.de/dt40est.html>.  
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US-10-755-889-18 (1-706) x AJ441866 (1-798)

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QY 487 GIuMeTcYsLeuHiStHAlAGLyProThrPheAlAGIuMeRGlyGIuThRGInSeR 506  
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QY 507 GIuTySeRSeAPSeSeRSeCySGIuAnGIyAlAPhePheCySaenGIuCySaSPCySaRG 526  
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Job time : 4896 secs

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GenCore version 5.1.7  
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Run on: March 2, 2006, 01:02:20 ; Search time 336 Seconds  
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3734.996 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 2606114

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	3793	99.2	3720	US-08-074-967-1	Sequence 1, Appli
4	3763	99.2	3720	US-08-553-541B-1	Sequence 1, Appli
5	3763	99.2	3720	US-09-268-202-1	Sequence 1, Appli
6	3763	99.2	3720	US-09-761-117-1	Sequence 1, Appli
7	3763	99.2	3720	PCR-US94-06669-1	Sequence 1, Appli
8	621.5	16.4	2769	US-09-620-312D-309	Sequence 309, App
9	614.5	16.2	2680	US-09-063-035-1	Sequence 1, Appli

10	540	14.2	2289	3	US-09-949-016-1780	Sequence 1780, Ap
11	508	13.4	2184	3	US-09-949-016-4402	Sequence 4402, Ap
12	503	13.3	3052	3	US-10-104-047-959	Sequence 959, App
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17	491	12.9	1892	2	US-08-933-750C-66	Sequence 66, Appl
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44	461.5	12.2	1833	3	US-10-104-047-1491	Sequence 1491, App
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#### ALIGNMENTS

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Sequence 3, Application US/09418640  
Patent No. 6140125  
GENERAL INFORMATION:  
APPLICANT: Jennifer K. Taylor  
TITLE OF INVENTION: ANTISENSE MODULATION OF BCL-6 EXPRESSION  
FILE REFERENCE: RRS-0102  
CURRENT APPLICATION NUMBER: US/09/418,640  
CURRENT FILING DATE: 1999-10-15  
NUMBER OF SEQ ID NOS: 89  
SEQ ID NO 3  
LENGTH: 3536  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURES:  
NAME/KEY: CDS  
LOCATION: (328) ..(2448)  
US-09-418-640-3

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Best Local Similarity: 100.0%  
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DB: 3  
Gaps: 0

US-10-755-889-18 (1-706) x US-09-418-640-3 (1-3536)

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Qy 541 HisSerAspIlySerProTyrIlyCysAspArgCysGlnAlaSerPheArgTyrIlySerGlyAen 560  
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US-09-814-915A-90  
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; Patent No. 6750015



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; GENERAL INFORMATION:
; APPLICANT: Horwitz, Kathryn
; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
; FILE OF INVENTION: Theteto
; TITLE REFERENCE: 2848-39
; CURRENT APPLICATION NUMBER: US/09/814,915A
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/214,870
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 90
; LENGTH: 3536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-915A-90

Alignment Scores:
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Score: 3793.00 Matches: 706
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-755-889-18 (1-706) x US-09-814-915A-90 (1-3536)

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QY 21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValIleValIleValSerArg 40
DB 388 AACCTTAATCGTCTCCGAGTCCGAGACATCTTGACTGATCTTGATCTGATCTGAGCGCT 447
QY 41 GluGlnPheArgAlaHisLeuThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle 60
DB 448 GAGCAGTTTACAGCCCATTAACACGGTCCCTCATGCGCTCAGTGGCTGTCTTATAGCATTC 507
QY 61 PheThrAspGlnLeuLeuCysAsnLeuSerValIleAsnLeuAspProGlnIleAsnPro 80
DB 508 TTTCACAGCCAGTGAATGCAACCTTAGTGTGATCAATCTAGATCTGAGATCAACCTT 567
QY 81 GluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGlyIle 100
DB 568 GAGGAGTTCGATCTCTGAGCTTCATGTCACATCTCGGCTCAATTGGGAGAGGC 627
QY 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGlnHisValIleAspThr 120
DB 628 AACATCAAGCGCTGATAGGCCACGCGCTATGTAACCTGAGATGAGACATGTTGTGAGACT 687
QY 121 CysArgIlePheIleLeuAlaSerGlnAlaGluMetValSerAlaIleLeuProProArg 140
DB 688 TGCCCGAAGTTATTAAGGCCAGTGAAGAGAGATGTTCTGTCATCAAGCTCTCTGCT 747
QY 141 GluGlnPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160
DB 748 GAAAGGTTCTCAACAGCGCGAGTGTGAGTCCCAAGACATATGAGCTTATGCGGAGTCT 807
QY 161 GluValIleGluAsnAsnLeuProLeuArgSerAlaProGlyCysGlnSerArgAlaPhe 180
DB 808 GAGGTGTGTGAGAACACCTGCACTGAGAGAGCGCGCTGCTGTGAGAGAGAGAGAGAGAG 867
QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
DB 868 GCCCCAGCGCTGTACAGTGTGCTGTCACACCGCAGCGCTCTTATTTCCATGACAGCAC 927
QY 201 LeuProValSerSerLeuLeuPheSerArgGlnGluPheArgAspValArgMetProVal 220
DB 928 CTCCTCGTAGAGCGCTCTCTTCTCCAGTGAAGAGTTCGGAGATGTCGGAGATGCTGTG 987
QY 221 AlaAsnProPheProLeuArgAlaLeuProCysAspSerAlaArgProValProGly 240

DB 988 GCCAACCCCTTCCCAAGAGAGGGGCACTCCATGTATAGTCCAGGCGCAGTCCCTGGT 1047
QY 241 GluTyrSerArgProThrLeuGlnValSerProAsnValCysHisSerAsnIleTyrSer 260
DB 1048 GAGTACAGCGCGCGGCTTGTGAGGTGTCCCTCCCAATGTGTGACACGACATATCTATTA 1107
QY 261 ProGlyGlnThrIleProGlnGlnAlaArgSerAspMetHisTyrSerValAlaGlyIle 280
DB 1108 CCAAGAGAAACATCCCAAGAGAGGACAGAGATGATGTGACATCACTGATGTGGTGAAGGC 1167
QY 281 LeuLeuProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLeuAlaSer 300
DB 1168 CTCAACTCTGCTGCCCCCTCAGCGCCGAAATGCCCTCACTCTCTGTGACAGGCGCAGC 1227
QY 301 LysGlnGlnGluArgProSerSerArgIleAspGlnIleAlaLeuHisPheGluProProAsn 320
DB 1228 AAGAGAGAGAGAGAGAGCTCTCGAAGATGATGTGCTCGCATTTTCGAGCCGCCAAT 1287
QY 321 AlaProLeuAsnArgIleGlyLeuValSerProGlnSerProGlnLysSerAspCysGln 340
DB 1288 GCACCCCTGAACGGAGAGGTCTGTGTTAGTCCACAGAGCCCCCAAGAAATCTGACTGACAG 1347
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QY 361 SerProProAlaLysSerProThrAspProLysAlaCysAsnTyrLysTyrLysPhe 380
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QY 381 IleValLeuAsnSerLeuAsnGlnAsnAlaLysProGlyIleProGlnGlnAlaGluLeu 400
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QY 401 GlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProProMetGluPro 420
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DB 1588 GAGAACTTGACCTCCAGTCCCAACCAAGTGTGAGCGAGGAGAGAGAGAGAGAGAGAGAG 1647
QY 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460
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QY 461 SerSerGlnSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480
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QY 481 GlnSerProGlnHisAlaGlnMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500
DB 1768 CAGTTCCTCAGCAGATGAGAGATGTGCTCCACAGCGGTGCGCCAGTTTGCTGAGAGAG 1827
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DB 1828 ATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1887
QY 521 AsnGluCysAspArgPhePheSerGlnGlnAlaSerLeuLysArgHisThrLeuGlnThr 540
DB 1888 AATGAGTGTGATCCCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1947
QY 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560
DB 1948 CACGTGACAAACCTTACATGATGTGACCGCTGCGAGGCTCTCTCGCTTACAGAGAGAG 2007
QY 561 LeuAlaSerHisLysThrValHisThrGlyGluLysProTyrArgCysAsnIleCysGly 580
DB 2008 CTCGCGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2067
QY 581 AlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgIleHisSerGlyGluLys 600
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Db 2068 GCCAGTTCACCGGCGAGCAACTGAAACCCACACTGATTCAGTCTGGAGAG 2127  
Qy 601 ProTyrIlyeCysegluThrCysegluAlaArgPheValGlnValAlaHisIleuAlaHis 620  
Db 2128 CCTCAAAAGCCAAACCTGCGAGCGACATTTGTACAGTGGCCCACTCCCTGCCAT 2187  
Qy 621 ValIeuIleHisThrIlygluIlyProTyrProCysegluIleCysegluThrArgPheArg 640  
Db 2188 GTGCTTATTCACACTGTGTGAGAGCCCTATCCCTGTGAATCTGTGGACCCCTTTCCG 2247  
Qy 641 HisIeuGlnThrIleuIlySerHisIleuArgIleHisThrIlygluIlyProTyrHisCyse 660  
Db 2248 CACCTTCAGACTCTGAAAGAGCACTGCGAATCCACAGAGAGAAACCTTACATTTG 2307  
Qy 661 GluIlyeCyseAnleuHisPheArgHisIlySerSerGlnleuArgleuHisIleuAlaGlnIly 680  
Db 2308 GAGAAAGTAACTGCACTTCCGTCCACAAAGCCAGCTGCGACTTCACTTCCCGCAAG 2367  
Qy 681 HisGluValAlaIleThrAnThrIlyValGlnTyrArgValSerAlaThrAspLeuProPro 700  
Db 2368 CATGGCGCCATCCACCAACACCAAGTGCATACCGGCTGACGCACTGCTGCC 2427  
Qy 701 GluLeuProIlySAlaCyse 706  
Db 2428 GAGCTCCCAAGCTTC 2445

RESULT 3  
US-08-074-967-1  
Sequence 1, Application US/08074967  
Patent No. 5641672  
GENERAL INFORMATION:  
APPLICANT: Dalla-Favera, Riccardo  
APPLICANT: Chasanti, R.S.K.  
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS  
TITLE OF INVENTION: bcl-6  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/074,967  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/43771  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3720 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 328..2445  
US-08-074-967-1

Alignment Scores:

Pred. No.:	5,12e-277	Length:	3720
Score:	3763.00	Matches:	701
Percent Similarity:	99.4%	Conservative:	1
Best Local Similarity:	99.3%	Mismatches:	4
Query Match:	99.2%	Indels:	0
DB:	2	Gaps:	0

US-10-755-889-18 (1-706) x US-08-074-967-1 (1-3720)

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Qy 21 AsnLeuAsnArgIleuArgSerArgAspIleIleuThrAspValIleValIleSerArg 40  
Db 388 AACCTTAATGCTCTCCGAGTGAAGACATCTTGAATGATGTGTGATCTTGTGAGCCGT 447  
Qy 41 GluIlePheArgAlaHisIlyeThrValIleuMetAlaCyseSerGlyLeuPheTyrSerIle 60  
Db 448 GAGCATTTAGAGCCCATTAACGGTCCATAGGCTGGAGAGGCTGTTATAGCATC 507  
Qy 61 PheThrAspGlnleuIlyeCyseAnleuSerValIleAsnleuAspProGluIleAsnPro 80  
Db 508 TTACAGACCAAGTGAATGCAACCTTAGTGAATCAATCTGATCTGAGATCAACCT 567  
Qy 81 GluGlyPheCyseAlaIleuIleuAspPheMetTyrThrSerArgIleuAsnleuArgGluIly 100  
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Db 628 AACATCATGGCTGTGATGAGCCAGGCTATGACTGAGATGAGACATGTGTGACACT 687  
Qy 121 CyseArgIlyPheIleIlyeAlaSerGluAlaGlnMetValSerAlaIleIlyePheProArg 140  
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Qy 161 GluValIleAlaAsnAsnleuProIleuArgSerAlaProGlyCyseGluSerArgAlaPhe 180  
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 Db 508 TTACAGACCAAGTTGAATGCAACCTTAGTGATATCAATTAATCTAGATCAACCTT 567  
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 Qy CysArgLysPheIleLysAlaSerGluAlaGluMetValSerAlaIleLysProProArg 140  
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 Db 808 GAGGTGTGAGAAACAACCTGCACTGAGAGAGCGCCCTGCTGTGTGAGACAGACGCTTT 867  
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 Db 1408 TCCCTCTCAGCAAGAGCCCACTGACCCCAAAACCTGCGAGCTGGAAGAAATCAAGATTC 1467  
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 Db 1468 ATGTGTCTCAACAGCTCTCAACCAAGATGCCAAACCAAGGGGGCTGTGAGCGCTGAGCTG 1527  
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Qy 421 GluAsnLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIle 440  
 Db 1588 GAAACCTTTGACTTCAGTCCAGTCCCAACCAAGCTGAGTGCAGCGGGAGGACTCCACCATC 1647  
 Qy 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460  
 Db 1648 CCACAAGCCAGCGGCTCAATTAATCGTTTAAACAGTCCATGACGAGCGGCTCTCCCGCAGC 1707  
 Qy 461 SerSerGluSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480  
 Db 1708 AGCAGGAGAGGCACTTACCACTTACATGACCCCCCGAAGTGCACGTCTCGGGCTT 1767  
 Qy 481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500  
 Db 1768 CAGTCCCAACAGATGAGAGATGTGCTCCACACCGCTGGCCCCACGTTCCCTGAGAG 1827  
 Qy 501 MetGlyGluThrGlnSerGluTyrSerAspSerSerCysGluAsnGlyAlaPheMetCys 520  
 Db 1828 ATGGGAGAGAACCCAGCTGAGTACATCAGATTTACTGCTGTGAAACGGGGCTTCTTTCG 1887  
 Qy 521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540  
 Db 1888 AATGAGTGTGACTGCGGCTTCTGTGAGAGGCTCACTCAAGAGGCAACGCTGCAAGACC 1947  
 Qy 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560  
 Db 1948 CACAGTGAACAACTCAACAAGTGTACGCGCTCCAGGCTCTTCCGCTACAAAGGCAAC 2007  
 Qy 561 LeuAlaSerHisLysThrValHisThrGlyGlyLysProTyrArgCysAsnIleCysGly 580  
 Db 2008 CTCGCGAGCACAAGACCTCTCATACCGGTGAAACCTTATCGTTGCAACATCTGTGTGG 2067  
 Qy 581 AlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgIleHisSerGlyGlyLys 600  
 Db 2068 GCCAGTTAAACGGGCAAGCCCACTGAAACCCACATCGAATTCATCTTGAGAGAGAG 2127  
 Qy 601 ProTyrLysCysGluThrCysGlyAlaArgPheValGlnValAlaHisLeuArgAlaHis 620  
 Db 2128 CCTCAAAATGGGAAACCTGCGGAGCAGATTTGTATCAGGTGGCCCACTCCGTGCCAT 2187  
 Qy 621 ValLeuIleHisThrGlyGlyLysProTyrProCysGluIleCysGlyThrArgPheArg 640  
 Db 2188 GTGCTTATCAACCTGTGTGAGAGCCCTTATCCCTGTGAAATGTGTGGCACCGGTTCGCG 2247  
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 Db 2248 CACTTCAGACTCTGAAGGCCACTGCGAATTCACACAGAGAGAACTTATCCATGTGT 2307  
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 Qy 681 HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700  
 Db 2368 CATGGCGCATCACCAACCAAGGTGCAATACCGGTGTGAGCCACTGACTGCTCCG 2427  
 Qy 701 GluLeuProLysAlaCys 706  
 Db 2428 GAGCTCCCAAGCCTGC 2445

RESULT 5  
 US-09-268-202-1  
 ; Sequence 1, Application US/09268202  
 ; Patent No. 6174997  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dalia-Favera, Riccardo  
 ; APPLICANT: Chaganti, Raju S.K.  
 ; TITLE OF INVENTION: CLOTHING AND USES OF THE GENETIC LOCUS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/268,202  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-2  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3720 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 328..2445.  
US-09-268-202-1

Alignment Scores:  
Pred. No.: 5.12e-277 Length: 3720  
Score: 3763.00 Matches: 701  
Percent Similarity: 99.4% Conservative: 1  
Best Local Similarity: 99.3% Mismatches: 4  
Query Match: 99.2% Indels: 0  
Gaps: 0

US-10-755-889-18 (1-706) x US-09-268-202-1 (1-3720)

1 MetAlaSerProAlaAspSerCysAlaGlnPheThrArgHisAlaSerAspValIleu 20  
328 ATGGCTCTGCGCGGCTGACAGCTGATCCAGTTCAACCCCATGCCAGGAGTCTTCTC 387  
21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValIleValIleValSerArg 40  
388 AACCTTAATGCTCCCGAGTCCGAGATCGAATCTTGAATGTTGATGTTGAGCCGT 447  
41 GlnGlnPheArgAlaHisIleValThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle 60  
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101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGlnHisValIleValAspThr 120  
628 AACATCATAGCTGCTGATGCGCAGCGCTATGTAACCTGAGATGAGCATGTTGTGAGCACT 687  
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141 GlnGlnPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg 160

748 GAGAGTCTCTCAACAGCCGAGATGATGATGCCCAAGATCATATGCTATCGGGTCTGT 807  
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808 GAGGTGTGAGAAACAACCTGCACTGAGAGAGCCCTGAGTGTAGAGCAAGACCTTT 867  
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988 GCCAACCCCTTCCCAAGAGCGGGCACTCCATGTGATGTGTCAGGCCAGTCCCTGTGT 1047  
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321 AlaProLeuAsnArgLeuArgIleValIleValSerProGlnIleValSerAspCysGln 340  
1288 GCAACCTCTGAACGGAAGGATCTGTGTTATGTCACAGAGCCCTCAAGAAATCTGATGCGCAG 1347  
341 ProAsnSerProThrArgIleValCysSerSerIleAsnAlaCysIleLeuGlnAlaSerGly 360  
1348 CCCAACTGCGCCACAGAGGCTGACAGCATGATGATCTGATCTCCAGAGGTTCTGCGC 1407  
361 SerProProAlaLysSerProThrAspProValAlaCysAsnTyrPheTyrIleValPhe 380  
1408 TCCCTCTCAACGAGCCCTCAACAGATGCAACCAAGGAGGCTGAGAGCTGAGCTG 1467  
381 IleValLeuAsnSerLeuAsnGlnAsnAlaLysProGlyGlnIleValIleValIleu 400  
1468 ATGCTGTCAACAGCTCTCAACAGATGCAACCAAGGAGGCTGAGAGCTGAGCTG 1527  
401 GlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProProMetGlnPro 420  
1528 GCGCGCTTTCCCAAGAGCTTACAGCGCCCACTGCTGCGAGCAACCATGAGAGCT 1587  
421 GlnAsnLeuAspLeuGlnSerProThrIleValLeuSerAlaSerGlyIleAspSerThrIle 440  
1588 GAGAACCTTGAACCTCCAGTCCCAACCAAGCTGATGCCAGCGGGAGGATCTCACCATC 1647  
441 ProGlnAlaSerArgLeuAsnAsnIleValIleAsnArgSerMetThrGlySerProArgSer 460  
1648 CCACAAACCCAGCCGCTCAATCAATGTTTAACAGTTCATGACAGGAGCTCTCCCGGAGGC 1707  
461 SerSerGlnSerHisSerProLeuTyrMetHisIleProProLysCysThrSerCysGlySer 480  
1708 AGCAGCAAGAGCACTACACTTATATGACACCCCGAAGTGCAGTCTGCGGCTCT 1767  
481 GlnSerProGlnHisAlaGlnMetCysLeuHisThrAlaGlyProThrPheAlaGlnGlu 500  
1768 CAGTCCCAACAGCATGACAGATGCTGCTCACACCCCTGCGCCCAAGTTCGCTGAGAGAG 1827  
501 MetCysGlnThrGlnSerGlnTyrSerArgSerSerCysGlnAsnGlyAlaPhePheCys 520



QY 241 GluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyrSer 260  
DB 1048 GAGTACAGCCGCGCGAGCTTGGAGGTGTCCCAATGTGTGCCACACCAATCTATCTATCA 1107  
QY 261 ProGluGlnThrIleProGluGluValArgSerAspMetHisTyrSerValAlaGluGly 280  
DB 1108 CCGAAGGAACAAATCCAGAAAGAGCGAGAGTATGTGCACTTCAATGTGTGGCTGAGGGC 1167  
QY 281 LeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLysAlaSer 300  
DB 1168 CTCAAACTCTGTGCCCCCTCAGCCCGAAATGCCCTTACTTCCCTTGTGACAGAGCCAGC 1227  
QY 301 LysGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAsn 320  
DB 1228 AAGAAGAGAGAGACCTCTCTCGAAGATGATGATTCCTCCGCAATTCGAGCCCCCAAT 1287  
QY 321 AlaProLeuAsnArgLysGlyLeuValSerProGlnSerProGluLysSerAspCysGln 340  
DB 1288 GCACCCCTGAACCGGAAGGGGTGTGTGTGTCACAGAGCCCCCGAAATCTGACTGCGAG 1347  
QY 341 ProAsnSerProThrGluAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSerGly 360  
DB 1348 CCAACTCTGCCCAAGAGGCTGTGACAGATGATGCTGTGCACTTCCAGGGCTTGTGGC 1407  
QY 361 SerProProAlaLysSerProThrAspProLysAlaCysAsnTyrLysTyrLysPhe 380  
DB 1408 TCCCTCTCAGCCAGAGAGCCCACTGAGCCCAAGCTGTGAGAAATACAAAGTTTC 1467  
QY 381 IleValLeuAsnSerLeuAsnGlnAsnAlaLysProGlyGlyProGluGlnAlaGluLeu 400  
DB 1468 ATCTGTCTCAACACCTCTCAACAGAAATGCCAAACAGGGGGGCTGTGACAGGCTGAGTG 1527  
QY 401 GluValGluSerProArgAlaTyrThrAlaProProAlaCysGlnProMetGluPro 420  
DB 1528 GGCGGCTTCTCCCAAGGCTTCAACGGGCCCACTGTGCTGCGACCACTGAGAGCT 1587  
QY 421 GluAsnLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyLysAspSerThrIle 440  
DB 1588 GAGAACTTGAACCTTCCAGTCCCAACCAAGCTGAGTGCACGGGAGAGACTCCACCATC 1647  
QY 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460  
DB 1648 CCAAGAGCCAGCCGCTCAATACATCTTAAACAGGTCTCAAGAGGGGCTCTCCCGCAGC 1707  
QY 461 SerSerGluSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480  
DB 1708 AGCAGCGAGAGCCACTCACTCACTACATGACCCCCGAAAGTGCACGTCTGCGACTCT 1767  
QY 481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500  
DB 1768 CAGTCCCAAGCATGAGATGATGTGCTCCACACCGGTGCGCCAGCTTGGCTGAGAG 1827  
QY 501 MetGlyGluThrGlnSerGluTyrSerAspSerSerCysGluAsnGlyAlaPhePheCys 520  
DB 1828 ATGGAGAGAGCCAGCTGAGTACTCAGATTTCTAGCTGTGAGAGCGGGGCTTCTTCTGCG 1887  
QY 521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540  
DB 1888 AATGAGTGTGACTGCGCTTCTCTAGAGAGGCTCACTCAAGAGGACACCGCTGAGACC 1947  
QY 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560  
DB 1948 CACAGTGAACAACCTTACAGTGTACCGGCTGCGAGGCTCTTCCGCTACAGAGGGCAAC 2007  
QY 561 LeuAlaSerHisLysThrValHisThrGlyGlyLysProTyrArgCysAsnIleCysGly 580  
DB 2008 CTGCGCAGCAGCAAAACCGTCCATACCGGTGAGAAACCTTATGCAACATCTGTGGG 2067  
QY 581 AlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgIleHisSerGlyGlyLys 600  
DB 2068 GCCCAGTTCAACCGGCGAGCCCAACTGAAACCCCACTCGAATTCACCTTGGAGAGAG 2127

QY 601 ProTyrLysCysGluThrCysGlyAlaArgPheValGlnValAlaHisLeuArgAlaHis 620  
DB 2128 CCTTCAAAATGCAAACTCGCGAGCCAGATTTGTACAGGTGSCCACTCGGTCCCAT 2187  
QY 621 ValLeuIleHisThrGlyGlyLysProTyrProCysGluIleCysGlyThrArgPheArg 640  
DB 2188 GTGCTTATCCACACTGCTGTGAGAGCCCTTATCCCTGTGAATCTGTGTGCAACCCGTTCCGG 2247  
QY 641 HisLeuGlnThrLeuLysSerHisLeuArgIleHisThrGlyGlyLysProTyrHisCys 660  
DB 2248 CACCTTCAAGCTTGAAGGCCCTGTGCAATCCACAGAGAGAACTTACCATTTGT 2307  
QY 661 GluLysCysAsnLeuHisPheArgHisLysSerGlnLeuArgLeuHisLeuArgGlnLys 680  
DB 2308 GAGAGTGTACTGCTGATTTCCCTCAAAAGCAGCTGTGACTTCACTTGGCCGAGAG 2367  
QY 681 HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700  
DB 2368 CATGGGCGCATCAACCAACCAAGTGCATACCGGCTGTGACCACTGACCTGCTCCG 2427  
QY 701 GluLeuProLysAlaCys 706  
DB 2428 GAGCTCCCAAGCCTGC 2445

RESULT 7  
PCT-US94-06669-1  
Sequence 1, Application PC/TUS9406669  
GENERAL INFORMATION:  
APPLICANT: Dalia-Favera, Riccardo  
INVENTOR: Chaganti, R.S.K.  
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/06669  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/074,967  
FILING DATE: 09-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 43771-A-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3720 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 328..2445  
PCT-US94-06669-1

Alignment Scores:



Pred. No.:	5,12e-277	Length:	3720
Score:	3763.00	Matches:	701
Percent Similarity:	99.4%	Conservative:	1
Best Local Similarity:	99.3%	Mismatches:	4
Query Match:	99.2%	Indels:	0
DB:	6	Gaps:	0

US-10-755-889-18 (1-706) x PCT-US94-06669-1 (1-3720)

QY	1	MetAlaSerProAlaAspSerCysAlaGlnPheThrArgHisAlaSerAspValLeuLeu	20
Db	328	ATGGCTCGCGGGCTGAGACGGCTGATTCAGTTACAGTCCCGCATGGCAGGAGATGTTCTTCTC	387
QY	21	AsnLeuAsnAlaGlyLeuArgSerArgAspIleLeuThrAspValValIleValIleSerArg	40
Db	388	AACTTAATCGTCTCCGGAGTGGACACATCTTGACTGATGTTCATTTGCTTTGTAGCCGT	447
QY	41	GluginPheArgAlaHisIleValThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle	60
Db	448	GAGCAGTTTAGAGGCCATTAATAACGGTCTCTAGCGCTTGAGAGAGCGCTGTTCTATAGCATC	507
QY	61	PheThrAspGlnLeuLeuPheCysAsnLeuSerValIleAsnLeuAspProGlnIleAsnPro	80
Db	508	TTTACAGACCGAGTTGAAATGCAACCTTGTGTGATTCATTCAGATCCCGAATCAACCTT	567
QY	81	GluGluPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly	100
Db	568	GAGGATTTCTGCATCTCTCGACTTCATGTCACATTCGGCTCAATTTGGGAGAGGC	627
QY	101	AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValIleAspThr	120
Db	628	AACATCATGGCTGTGATGAGCCACGGCTATGTACCTGCAGATGAGACATGTTGTGACACT	687
QY	121	CysAspGlyPheIleLeuAlaSerGluAlaGluMetValSerAlaIleIleArgProArg	140
Db	688	TGCCGGAAGTTATTTAAGCCACGTGAACAGAGAGATTTCTGCCATCAACCTCTCGCT	747
QY	141	GluGluPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg	160
Db	748	GAGAGTTCTCTACACGCCGAGATGCTGATGCCCCAGACATCATAGGCTTAATCGGGTCTG	807
QY	161	GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe	180
Db	808	GAGGTGGTGGAGAACAACTGGCACTGAGAGAGCGCCCTGGGTGTGAGAGCAGAGCTTT	867
QY	181	AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis	200
Db	868	GCCCCCAGCTGTATACGTGGCTCTGCCACCGCCAGCGCTCTTATTCATGTACAGCCAC	927
QY	201	LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspValArgMetProVal	220
Db	928	CTCCCTGTCAGAGCTCTCTCTTCTCCAGATGAGAGTTTCGGGATGTCGGATGCCCTTG	987
QY	221	AlaAsnProPheProGlyAsnArgAlaLeuProCysAspSerSerAlaArgProValProGly	240
Db	988	GCCAAACCTTCCCAAGAGGCGGCGACCTCCCATGTGATGTGCGCAGGCCAGTCCCTGCT	1047
QY	241	GluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyrSer	260
Db	1048	GAGTACAGCCGGCCGACATTGTGAGGTGTGCCCCCAATGTGTGCGCACAGCAAAATCATATTCA	1107
QY	261	ProTyrGluThrIleProGluGluAlaArgSerAspMetHisTyrSerValAlaGluGly	280
Db	1108	CCCAAGGAACATCCCGAAGAGGACGAAATGTATGTACCTACACAGTGTGCTTAGGGC	1167
QY	281	LeuTyrProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspIleValSer	300
Db	1168	CTCAAAACCTGCGCCCTCAGCCCGGAATGCCCTCACTTCCCTTGAGACAAGCCAGCC	1227
QY	301	IleGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProAsn	320
Db	1228	AAAGAGAAGACAGACCTCTCTCGAAGATGTGATTTGCCATTTGAGAGCCCCCAAT	1287

QY	321	AlaProLeuAenAglYsGlyLeuValSerProGlnSerProGlnIlySerAspGlyGln	340
Db	1288	GCACCCCTGAACCGGAAGGCTGTGGTTATGTCACAGAACCCCCAGAAATCTGACTGCCAG	134
QY	341	ProAsnSerProThrGlnValACysSerSerIlyAsnAlaCysIleLeuGlnAlaSerGly	360
Db	1348	CCCAACTGCCCCACAGAGGCTTCGACAGTAAATGCTGCACTCTCCAGGGCTTGGC	140
QY	361	SerProProAlaIlySerSerProThrAspProIlyValACysAsnTPILyIlySTyIlyPhe	380
Db	1408	TCCCCTCCAGACCAAGAGGCCCTCACTGACCCCAAGAGCTCACTGCGTGAAGAAATACAAATGTC	146
QY	381	IleValIleuAsnSerIleuAsnGlnAsnAlaIlySerProGlyGlyProGlnGlnAlaGlyIleu	400
Db	1468	ATCTGTGTCACACAGCTTCACCAAGATGTCACAAACCGAGGAGGCTGAGACAGCTAGCTG	152
QY	401	GlyIlyProIleuSerProAlaGlyAlaTyThrAlaProProAlaCysGlnProProMetGlyPro	420
Db	1528	GAGCGGCTTTCCCAACAGGCTTACAGGGCCCCACTGCTGCGACCAACCATGGAAGCT	158
QY	421	GluAsnIleuAspLeuGlnSerProThrIlyIleuSerAlaSerGlyGlyAspSerThrIle	440
Db	1588	GAGAACTTGACCTTCAGTCCCAAGCCCAAGCTGAGTGCAGGGGAGAGACTCCACACATC	164
QY	441	ProGlnAlaSerAlaGlyLeuAsnAsnIleValAsnAspSerMetThrGlySerProArgSer	460
Db	1648	CCACAGACCAACCGGCTCAATTAACATCTTTAAACAGTCCATAGACGAGGCTCTCCCGCAGGC	170
QY	461	SerSerGlnSerHisSerProLeuIlyzMetHisProPolsCysThrSerCysGlySer	480
Db	1708	AGCGACGAGGACCTCACTCAACTTCAATGCACCCCCGAAAGTGCACGTCTCGCGGCTT	176
QY	481	GlnSerProGlnHisAlaGlyMetCysLeuHisThrAlaGlyProThrPheAlaGlyGln	500
Db	1768	CAGTCCCAACGCAAGCAAGATGTGGCTCCACACCGGTGGCCCCAGCTTCGCTGAGAGAG	182
QY	501	MetGlyGlyThrGlnSerGlyIlyzSerAspSerSerCysGlyAsnGlyValaPhePheCys	520
Db	1828	ATGGGAGAGACCCAGCTCGAGTACTCAATCTTACTCTGTGAAGAGGGGCTTCTTCTTGC	188
QY	521	AsnGlyCysAspCysArgPheSerGlnGlnAlaSerLeuIlyAspArgHisThrIleuGlnThr	540
Db	1888	AATGATGTGACTGCCGCTTCTCTTGAAGGCTTCACTCAAGAGGACACGCTGCAGAC	194
QY	541	HisSerAspIlyProTyIlyAsCysAspArgCysGlnAlaSerPheArgTyIlyGlyAsn	560
Db	1948	CACAGTGAACAACCTTACAGTGTACCGGTGCGAGGCTCTTCGGTCAAGAGGCAAC	200
QY	561	LeuAlaSerHisIlyIyThrValHisThrGlyGlyIlyProTyArgCysAsnIleCysGly	580
Db	2008	CTGGCACAACCAAGACCGTCCATACCGGTGAGAAACCTTACGTGGCAACATCTGTGGG	206
QY	581	AlaGlnPheAsnArgProAlaAsnIlySerThrHisThrArgIleHisSerGlyGlyIlyS	600
Db	2068	GCCCAAGTTCAACCGGCACAGCCCAACTGAAGAACCCACACTCGAATTCATCTTGAGAGAAAG	212
QY	601	ProTyIlyCysGlyIlyThrCysGlyValaArgPheValGlnValAlaHisIleuArgAlaHis	620
Db	2128	CCCTACAAATGGGAACCTCGCGGAGACGAGATTTGTACAGTGTGGCCACCTCGGTGCCAT	218
QY	621	ValIleuIleHisThrGlyGlyIlyAspProTyProCysGlyIleCysGlyIlyThrArgPheArg	640
Db	2188	GTGGTTATTCACACTGTGTGAGAGCCCTATCCCTGTGAATCTGTGGCAACCGGTTCCGG	224
QY	641	HisIleuGlnThrIleuIlySerHisIleuArgIleHisThrGlyGlyIlyAspProTyHisCys	660
Db	2248	CACCTTCAGACTCTGAAGAGCCACTGCGCAATCCACACGAGAGAGAAACCTTACCATGT	230
QY	661	GlyIlyCysAsnIleuHisPheArgHisIlyIySerSerGlnIleuArgIleuHisIleuArgGlnIlyS	680
Db	2308	GGAAGTGTAACTGCTGATTTCCGTCAACAAAGCCAGCTGCGACTTCACTTGGCCGCAAGAG	236
QY	681	HisGlyAlaIleIyThrAsnThrIlyValGlnTyArgValSerAlaThrAspIleuProPro	700





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QY 427 rProthrlySLeuSerAlaSerGlyAluAspSerThrIleProGlnAlaSerArgLeuAs 447
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DB 1328 CCTACGGCTGCGAGAGTGGCGGAAAGACTACC-----GCCCTCATCAGCTGG 1375
QY 447 nAenIleValAsnArgSerMetThrGlySerProArgSerSerSerGlnSerHisSerPr 467
    |||||
DB 1376 CTGAACCTGCACAAAGAAAGCGGCACTGGGCGAGGCCGCTACCGCT---GCCAGAGACTGC 1432
QY 467 oLeuTYrMetHisProProlyeCySerHiser-----CySerGlySerG 481
    |||||
DB 1433 GCGAAGCTCTTCAACCACTCGGCGCAACTCAAGCGCCACAGCTGTGTGCACAGCGCGAG 1492
QY 481 nSerProGlnHisAlaGluMetCySerLeuHisThrAlaGlyProThrPheAlaGlu----- 499
    |||||
DB 1493 AAGCCCTTAC-CAGTGGCACTACTGC-----GGCGCGCTCTTCTCCAGACCCCAAC 1539
QY 500 -----GluMetGlyGluThrGlnSerGlnGlyTyrSerAspSerSerCy 513
    |||||
DB 1540 TTCCAAAGATGCCGCACTGTGAAGCCACGACGACGACAAAGAGCAAGATGCCACACTG 1599
QY 513 eGlu-----As 515
    |||||
DB 1600 CGACAAGAAATTCAACCAAGTAGAGGAACCTGAAGGCCCACTGAAGATCCACATCCGCTGA 1659
QY 515 nGlyAlaPhePhePheCysAsnGluCysAspCysArgPheSerGlnGluAlaSerLeuLysAr 535
    |||||
DB 1660 CGGGCCCCCTCAAGTGGCGAGTGTGGAAAGCAAGTTCACCACTCGGAGAACTGAAGCG 1719
QY 535 gHisThrLeuGlnThrHisSer---AspLysProTYrLysCysAspArgCysSerGlnAlaSe 554
    |||||
DB 1720 GCAC---CTTCGATGCACAGCGGGGAGAAAGCCCTAGTGTGATGCATCCACTGCCAGGACA 1776
QY 554 rPheArgTYrLysGlyAsnLeuAlaSerHisSlyThrValHisThrGlyGluLysProTY 574
    |||||
DB 1777 GTTTCAGACACCCCGGGGCTCTGACAGCGGCACTGCCCATTCACACAGGTGAAGAGCCATG 1836
QY 574 rArgCysAsnIleCysGlyAlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrAr 594
    |||||
DB 1837 CCAGTGTGTGATGTGGGTAAAGGCTTCACCCAGGCCAGTCCCTCATGCCCCACGCTGG 1896
QY 594 gIleHisSerGlyGlyLysProTYrLysCysGlnThrCysGlyAlaArgPheValGlnVa 614
    |||||
DB 1897 CCAAGCACACCGGGGAGAAAGCCCTACGTCGCGAGCCGCTGGCGAAGAGATTCCTCCAGTC 1956
QY 614 lAlaHisLeuValAlaHisValLeuIleHisThrGlyGluLysProTYrProCysGluI 634
    |||||
DB 1957 CAGCCAGTTGGCCCAATCATATTCGCCCAACCAACATCCGCCCAACAAAGTGCAGCGCT 2016
QY 634 eCysGlyThrArgPheArgHisLeuGlnThrLysSerHisLeuArgIleHisThrG 654
    |||||
DB 2017 GTCCAGCAAGAGCCCTCTGTAACGTTGGGGGAGCTGTGCCAAGCAATCATCTTCACTGG 2076
QY 654 yGluLysProTYrHisCysGlyLysCysAsnLeuHisPheArgHisLeuSerGlnLeuAr 674
    |||||
DB 2077 AGAAGAGCCTTACTCTGTGTATAGTGTGGCGGTTCACACCGGTTAAACAACACTGGC 2136
QY 674 gLeuHisLeuValGlnLysHisGlyAlaIleThrAsnThrLysValGlnIlyrArgValSe 694
    |||||
DB 2137 CTCGCCAGTGAAGACCTGCACACGAGGCAAGGCAAGCATCAAGATC----- 2182
QY 694 rAlaThrAspLeuProProGlu 701
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DB 2183 -----CTGGAGCCCGAG 2194

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RESULT 9  
US-09-063-035-1

Sequence 1, Application US/09063035  
Patent No. 616091  
GENERAL INFORMATION:  
APPLICANT: PEUKERT, Karen; HABENEL, Frank; and EILERS,  
APPLICANT: Martin  
TITLE OF INVENTION: Myc-binding zinc finger proteins,

```

/ TITLE OF INVENTION: their preparation and their use
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Kell & Weinkeuf
/ STREET: 1101 Connecticut Avenue
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.2 Mb storage
/ COMPUTER: IBM AT-compatible, 80486 processor
/ OPERATING SYSTEM: MS-DOS version 6.1
/ SOFTWARE: WordPerfect version 8.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/063,035
/ FILING DATE: 21-APR-1998
/ CLASSIFICATION: 514
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2680 base pairs
/ TYPE: Nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: 5'UTR
/ LOCATION: 1..159
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 160..2571
/ NAME/KEY: CDS
/ LOCATION: 2572..2680
/ US-09-063-035-1

Alignment Scores:
Pred. No.: 4,266-37 Length: 2680
Score: 614.50 Matches: 204
Percent Similarity: 40.9% Conservative: 102
Best Local Similarity: 27.3% Mismatches: 289
Query Match: 16.2% Indels: 154
DB: 3 Gaps: 25

US-10-755-889-18 (1-706) x US-09-063-035-1 (1-2680)
QY 9 lIeGlnPheThrArgHisAlaSerAspValLeuLeuAsnLeuAsnArgLeuArgSerArg 28
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DB 160 ATGAGCTTTCGCCAGCAGCCAGCATGTCTTGAAACAGCTGAACACAGCGGCGAGCTG 219
QY 29 AspIleLeuThrAspValValIleValAlaSerArgGluGlnPheArgAlaHisSlyThr 48
    |||||
DB 220 GGGCTCTCTGTGACTGCACCTTTGTGTGAGCGGTTCACCTTTAAAGGCTCATTAAGCA 279
QY 49 ValLeuMetAlaCysSerGlyLeuPheTYrSerIlePheThrAspGlnLeuLysCysAsn 68
    |||||
DB 280 GTGCTGGCGCGCTGCAGCGAGTACTTCAAGATGCTCTGTGTGACAG----- 327
QY 69 LeuSerValIleAsnLeuAspProGluIleAsnProGluGlyPheCysIleLeuLeuAsp 88
    |||||
DB 328 AAGAGCTGTGTGCACTGTGACATCACT---AACGGCGAGGCGCTGGCGAGATGCTGGAG 364
QY 89 PheMetTYrThrSerArgLeuAsnLeuArgGluGlyAsnIleMetAlaValMetAlaThr 108
    |||||
DB 385 TTATGTACAGCGCCAACTGAGCTGAGCCCTGAGCAAGGTGATGTGTGCGCGCTG 444
QY 109 AlaMetTYrLeuGluMetGlnHisValAlaAspThrCysArgLysPheIleLysAlaSer 128
    |||||
DB 445 GCGACTTCTCTCCAAATGACAGCATCATCAGCGGCTGCATGCCCTCAAGTCACTTGGCT 504
QY 129 GluAlaGluMetValSerAlaIleLysProProArgGluGluPheLeuAsnSerArgMet 148

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Db 505 GAG-----CCGGCTACCAAGCCT----- 522

Qy 149 LeuMetProGlnAsp11MetAla1TYrArg1YArg1Val1GluAsn1LeuPro 168

Db 523 -----GGGGAAAGCCGGAG 537

Qy 169 LeuArgSerAlaProGly1CyG1Ser1Arg1a-----PheAlaProSer1Leu 184

Db 538 GCCTTGCCCAAGAGAGGGAGACAGAGAGCCCAAGAGAGAAAGTGGCCCAAGACG 597

Qy 185 TyrSer-----GlyLeuSerThiPro-----ProAlaSerTyrSerMet 197

Db 598 CTGAGCAGAGCTCGAGACGAGACGAGACACCCATAGGCCCCACG----- 645

Qy 198 TyrSerHisLeuProValSerSer1Leu1PheSerAsp1Glu1PheArgAspValArg 217

Db 646 -----AGGACCTCAAG 657

Qy 218 MetProValAlaAsnProPhePro1Glu1Arg1Ala1LeuPro1Cy1AspSerAla1ArgPro 237

Db 658 -----GAGAGGGCCGGCTCAGGCCCAAGAGTGGCCAGC 693

Qy 238 ValProGly1Glu1TyrSerArgProThiLeuGluValSerProAsnVal1CyHisSerAsn 257

Db 694 GGTGCAGACGACAGACAGAAAGCCGAT----- 720

Qy 258 IleTyrSerPro1Glu1Thi1LePro1Glu1Ala1ArgSerAspMetHis1TyrSerVal 277

Db 721 -----GGGCCCCGGGAGCCCGCGCTGTGAGCTCAAGCCAGACCCCAAGTGGCATG 774

Qy 278 AlaGluGlyLeu1YrPro1Ala1ProSerAla1ArgAsnAla1Pro1TyrPhePro1CyAsp 297

Db 775 GCTGCCGAGAAAGCTGAGCGCGCTTTGCTCCAGAGCTCGAGCAAGAAATGAGAGTGGAG 834

Qy 298 LysAlaSer1YrGlu1Glu1ArgProSerSerGluAspGlu1Leu1His1PheGlu 317

Db 835 CCGCGCCGGAAGGGGAAAGAGAGCAAAAGAGACAGAGAGAGCAAGAGAGAGGGCCGA 894

Qy 318 ProProAsnAla1Pro1LeuAsnArg1YrGly-----LeuValSerPro1GlnSerPro1Gln 335

Db 895 GGGCCA---GCTGAGCTCAAGAGAGAGGGTTCACGCTGGAGAAACGAGAGAGCCCGCAG 951

Qy 336 LysSerAspCyG1nProAsnSerProThi-----GluAla1CySerSer-Ly 351

Db 952 GAGAAACGAGAAATGAGAGTACAGCGGGACAGACTCGGGCGAGAGCTCGCTCCGAGGCG 1011

Qy 351 AsnAla1Cy1Leu1Gln1Ala1SerGlySerProProAla1YrSerProThiAspPro1Y 371

Db 1012 CGGGGCTCGCGCTCAGGACCTACCGGCGACCGACGAGTCCMAAGGCTTACGCTCGCTC 1071

Qy 371 Ala1CyAsn1Arg1Yr1Yr1Yr1Phe1Leu1Leu1Asn1Ser1Leu1Asn1Ala1Y 391

Db 1072 ATCCACAAAGTGGAGG-----ACTGTGGAGAGAGTTACCGCACACGGGGAGAC 1119

Qy 391 sPro1Gly1Pro1Glu1Gln1Ala1Glu1Leu1YrArg1LeuSerProArgAla1YrThiAla-- 410

Db 1120 TTCAGACGGCACATCCGATTCACACGGGGGAGAGCCCTTCTCGTCCGGGAGAGCGAGC 1179

Qy 411 ----ProProAla1CyG1nPro1ProMetGluPro-----GluAsnLeuAsp1Leu1nSe 427

Db 1180 AAGGCTTTTCGACCGGCGCCGTCGAAAGCCCTTGAGAAAGCCACAGCCCTTTGAG 1239

Qy 427 rProThi1Yr1LeuSerAlaSerGly1Glu1AspSerThi1LePro1Gln1AlaSerArg1LeuAs 447

Db 1240 CCTTACGGCTGGAGAGAGTGGGGAAGACTAC-----GCTCATACAGCCTG 1287

Qy 447 Asn1LeuValaAsnArgSerMetThi1YrSerProArgSerSerSerGluSerHisSerPr 467

Db 1288 CTGAACCTGCACAAAGAGCGGCACTCGGGCGAGGCGCTACCGCT---GCCAGAGACTGC 1344

Qy 467 Oleu1YrMetHisProPro1Yr1Cy1ThiSer-----CyG1YrSerG1 481

[illegible]





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Db      1171 ATGGACTTCAGCACCTATGGGGGCTGCTGCCAGGCTTCATCCAGAGGACTGTTTC 1230
      :|||:|||||:|||||:
Qy      444 SerArgLeuAsnAniLeValAsnArgSerMetThrGlySerProArgSerSerGlu 463
      :|||:|||||:|||||:
Db      1231 AGCAAGCTGGGGAGCTGGCT---GTGGCATGAAAGTACAGAGCCGACCACTCGAGAG 1287
      :|||:|||||:|||||:
Qy      464 SerHisSerProLeuThrMetHisProProLysCysThrSerCysGlySerGlnSerPro 483
      :|||:|||||:|||||:
Db      1288 -----CAGTGCAGCGTGTGTGGGCTTCAGCTTCCCT 1317
      :|||:|||||:|||||:
Qy      484 -----GlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPhe 497
      :|||:|||||:|||||:
Db      1318 GATTAAGAGGCTGTGAGCAGCAGAGAG---CTGCACAGTGGATGAAGAAGTAC 1371
      :|||:|||||:|||||:
Qy      498 AlaGluGluMetGlyLthrGlnSerGlyLysSerAspSer----- 511
      :|||:|||||:|||||:
Db      1372 GGGTGCAGGCTC-----TCCGGGAAGCCGGTTCCTGGATGATTGGCGGCTGAGAAATGCAC 1425
      :|||:|||||:|||||:
Qy      512 -----SerCysGluAsnGlyAlaPhePheCysAsnGluCysAspCysArgPhe 527
      :|||:|||||:|||||:
Db      1426 TTACTGGCTCATTCAGCGGCTGCCAAGACCTTGTCTGTGATGATGCGGTGCACAGTTT 1485
      :|||:|||||:|||||:
Qy      528 SerGluGluAlaSerLeuLysArgHisThrLeuGlnThrHis-----SerAspLysPro 545
      :|||:|||||:|||||:
Db      1486 TCGAAGAGGATGCCCTCGAGACACACAGG---CAGACCATCTGGCACTGACATGGCC 1542
      :|||:|||||:|||||:
Qy      546 TyrLysCysArgArgCysGlnAlaSerPheArgTyrLysGlyValAsnLeuAlaSerHisLys 565
      :|||:|||||:|||||:
Db      1543 GTCTTGTGTGCTGTGTGTGGGAAGCGCTTCACAGCCGACAGCCGACCTGCAGCAGCACATG 1602
      :|||:|||||:|||||:
Qy      566 ThrValHisThrGlyGluLysProTyrArgCysAsnLeuCysGlyAlaGlnPheAsnArg 585
      :|||:|||||:|||||:
Db      1603 GAGGTCCACCGCGGCTGCCACGCTACATCTGCAAGTAGTCAACGCCACCTTCCCGACG 1662
      :|||:|||||:|||||:
Qy      586 ProAlaAsnLeuLysThrHisThrArgLysHisSerGlyGluLysProTyrLysCysGlu 605
      :|||:|||||:|||||:
Db      1663 CACACGGCTCTCAAAACCCACCTGCGCTCACAATACAGGCGAACCCCTACAGTGTGAG 1722
      :|||:|||||:|||||:
Qy      606 ThrCysGlyAlaAlaArgPheValGlnValAlaHisLeuArgLysHisValLeuLysHisThr 625
      :|||:|||||:|||||:
Db      1723 TTCTGTGGCAGTGTCTCCGGAGTAGAGCACACTCAAGAGCCACAACCATCCACAGC 1782
      :|||:|||||:|||||:
Qy      626 GlyGluLysProTyrProCysGluLysCysGlyThrArgPheArgHisLeuGlnThrLeu 645
      :|||:|||||:|||||:
Db      1783 GGTGAAGAACCTTACAGATGCATGCTGTGGCAGGAAGTTCAAGCTTCAAGCATCAGCTG 1842
      :|||:|||||:|||||:
Qy      646 LysSerHisLeuArgLysHisThrGlyGluLysProTyrHisCysGlyLysCysAsnLeu 665
      :|||:|||||:|||||:
Db      1843 GAGACGCACTATAGGGTGCACACAGGTGAAGAGCCCTTGAAGTGTAGCTCTGCACAG 1902
      :|||:|||||:|||||:
Qy      666 HisPheArgHisLysSerGlnLeuArgLeuHisLeuArgGlnLysHisGlyAla 683
      :|||:|||||:|||||:
Db      1903 CGCTCCGGGACTACTCGGCCATGATCAGACCACTGAGAAAGCACAACGGCGCC 1956
      :|||:|||||:|||||:

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US-10-104-047-959
Alignment Scores:
Pred. No.: 1,64e-28 Length: 3052
Score: 503.00 Matches: 190
Percent Similarity: 35.5% Conservative: 83
Best Local Similarity: 24.7% Mismatches: 265
Query Match: 13.3% Indels: 232
DB: 3 Gaps: 34

US-10-755-889-18 (1-706) x US-10-104-047-959 (1-3052)
Qy      33 AspValAlaIleValAlaSerArgGluGlnPheArgAlaHisLysThrValLeuMetAla 52
      :|||:|||||:|||||:
Db      294 GATGTGGCTGTGTCTTCTCCAGGAGGAACTCGCA-----CTGCTCATCTTACC 344
      :|||:|||||:|||||:
Qy      53 CysSerGlyLeuPheThrSerLeuPheThrArgGlnLeuLysCysAsnLeuSerValIle 72
      :|||:|||||:|||||:
Db      345 CAGAGGAAGCTGTACCGAGATGTCATGTGTGAGAACTTCAG---AACCTGGTGCAGTG 401
      :|||:|||||:|||||:
Qy      73 AsnLeuAspProGluLysAsnProGluGlyPheCysIleLeuLeuAspPheMetTyrThr 92
      :|||:|||||:|||||:
Db      402 GGGCATCTTCCC---TTCCAAACCAAT-----ATGGA 431
      :|||:|||||:|||||:
Qy      93 SerArgLeuAsnLeuArgGluGlyValAsnIleMetAlaValMetAlaThrAlaMetTyrLeu 112
      :|||:|||||:|||||:
Db      432 TCCCAATTGGAAGCAGAAAGAAAGCTTGGATGATGAAACAGAAACCAAGAAAGACAGC 491
      :|||:|||||:|||||:
Qy      113 GlnMetGluHisValAlaAspThrCysArgLysPhe----- 124
      :|||:|||||:|||||:
Db      492 AAGCATCAAAATGAATGGAACACTCCAAAATTTGCAATTAATACCTTTCAATCAA 551
      :|||:|||||:|||||:
Qy      124 ----- 124
      :|||:|||||:|||||:
Db      552 GAGCTGTCTGCTGGCAATCTGAAACAGGTTGCAAGTAATTAACAGGTGCTTCAG 611
      :|||:|||||:|||||:
Qy      125 -----IleValAserGluAlaGluMet--- 132
      :|||:|||||:|||||:
Db      612 GGGAAGTTCACAGTATTACAGGTGACTGATTCAGTTTCTGAAATGAGAACAT 671
      :|||:|||||:|||||:
Qy      133 -----ValSerAlaIleLysProProArgGluGluPhe----- 143
      :|||:|||||:|||||:
Db      672 ATATGAACCTTAAGAGAGATAGCTCTATTATTGAAATCAAGAGTTTCCATTTGG 731
      :|||:|||||:|||||:
Qy      144 -----LeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArg 158
      :|||:|||||:|||||:
Db      732 AGAACCCAGCATTTCTTCCGGAATACATATCTGAGTAGTACACAGATTCAAGT---AAG 788
      :|||:|||||:|||||:
Qy      159 GlyArgGluVal---ValGluAsnAsnLeuPro-----LeuArgSerAla 172
      :|||:|||||:|||||:
Db      789 GGTAAACAATTTGATCTGAAAATTAACCTGCAAAATGACGAAAGACTTTCATGAAGAAATCA 848
      :|||:|||||:|||||:
Qy      173 ProGlyCysGluSerArgAlaPheAlaProSerLeuTyrSerGlyLeuSerThrProPro 192
      :|||:|||||:|||||:
Db      849 CCA-----TTTCATGAGCATATTAAACTGACACAGAACCAAAACCC 890
      :|||:|||||:|||||:
Qy      193 AlaSerTyrSerMetTyrSerHisLeuProValSerSerLeuLeuPheSerAspGluGlu 212
      :|||:|||||:|||||:
Db      891 TCGAAAGTATATATATGCAAA-----ATCATGTAGTAGTGCCTC 932
      :|||:|||||:|||||:
Qy      213 PheArgAspValArgMetProValAlaAsnProPheProLysGluArgAlaLeuProCys 232
      :|||:|||||:|||||:
Db      933 -----AACCAAGAAATTTACCTTAAAGAA-----GAGAAACCCCATCATGT 971
      :|||:|||||:|||||:
Qy      233 AspSerAlaArgProValProGlyGlyLysSerArg-----ProThrLeu 247
      :|||:|||||:|||||:
Db      972 -----GGTGAAGTGTGAAGGGCTTCAGTTATAGCCCAAGGCTT 1010
      :|||:|||||:|||||:
Qy      248 GluValSerProAsnVal-----Cys-----HisSerAsnIleTyr 259
      :|||:|||||:|||||:
Db      1011 CCCCTTCATCCGATATGTTCACACAGAGAAATGCTTCACTGATTAAGCTTCATCTGGCA 1070
      :|||:|||||:|||||:
Qy      260 SerProLysGluThrIleProGluGluAlaArgSerAspMetHisTyrSerValAlaGlu 279
      :|||:|||||:|||||:

```



QY	5	AlaIspSerCysIleGlnPheThrArgHisAlaSerAspValLeuLeuMetLysAsnArg	24
DB	75	TCTGATATCAAAATGAGATTGGACCACTGTGAGCACCTTTAGAGACTGAACAATA	134
QY	25	LeuArgSerArgAspIleLeuThrAspValValIleValValSerArgIleGlnPheArg	44
DB	135	CAGCGGGAAGCAGGTTTCTCTGTGACTGTACCATAGTATGATGGGAATTCAGATTAA	194
QY	45	AlaHisIleuThrValLeuMetAlaCysSerGlyLeuPheTyrSerIlePheThrAspGln	64
DB	195	GCTCATAGGAATGTCTGGCTGGCTCTTTATGTAGTATTTTGGTGGCATCTACAGAACACT	254
QY	65	LeuIleuCysAsnLeuSerValIleAsnLeuAsp---ProGluIleAsnProIleGlyPhe	83
DB	255	TCTGAGCAACAT-----GTCCTTCTTGATCAGAGTCAGGTGAAGCTGATGATTT	305
QY	84	CysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgIleGlyAsnIleMet	103
DB	306	CAGAAACGTGTGAGTTTATATACACAGAACCTTTAAATCTTGACAGTTGGATGTTTAA	365
QY	104	AlaValMetAlaThrAlaMetTyrLeuGlnMetGlnHisValValAspThrCysArg---	122
DB	366	GAAATTCATCAGCGTGTCTACTATCTCAAAAGTGGAGAGGTGCTCACTAAATGCAATA	425
QY	123	-----LysPheIleuYsaIserGluAlaGluMetValSerAlaIleuYs	137
DB	426	AAGATGGAAGATTTTGCTTTATTTGCTATTCCTTTCTACAGAGATATCTAGTATTA	485
QY	138	ProProIaArgIleGlnIleuPheLeuAsnSerArgMetLeuMetProGluAspIleMetAlaTyr	157
DB	486	GGAAACATTGAA-----TTGAATCAACAGACTTGTCTT-----	518
QY	158	ArgGlyArgGluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGlnSer	177
DB	519	-----CTTACTCTGGAGAT-----	533
QY	178	ArgAlaPheAlaProSerLeuTyrSerGlyLeuSerThrProAlaSerTyrSerMet	197
DB	533	-----	533
QY	198	TyrSerHisLeuProValSerSerLeuPheSerAspGluIlePheArgAspValArg	217
DB	534	-----TATATATATCGAAGAAATCGAAGATATCT	563
QY	218	MetProValAlaAsnProPheProlysgIuArgAlaLeuProCysAspSerAlaArgPro	237
DB	564	ACAGATTGATTACAGCAATCTTAACAAGGCGCTTA-----	602
QY	238	ValProGlyGluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsn	257
DB	602	-----	602
QY	258	IleTyrSerProIleGluThrIleProGluGluAlaArgSerAspMetHisTyrSerVal	277
DB	602	-----	602
QY	278	AlaGluGlyLeuIleProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAsp	297
DB	603	-----GCGAAA	608
QY	298	LysAlaSerIleGluIleGluIleArgProSerSerGluAspGluIleAlaLeuHisPheGlu	317
DB	609	AGGTCTCTCAACGAAAGAAAGAAAGAGGCT-----TTCAAC	647
QY	318	ProProAsnAlaProLeuAsnArgIleGlyLeuValSerProGlnSerProGlnIleYsSer	337
DB	648	TCCCGCAAAAACAGCGCAATTA-----ACAGTGCATATGCC-----AGT	689
QY	338	AspCysGlnProAsnSerProThrGluAlaCysSerSerIleAsnAlaCysIleLeuGln	357
DB	690	GACATCTTAGAGATGATCTGTTGAATTAATTCCTAGATCAAT-----	734

Oy	358	AlaSerGlySerProProAlaLysSerProThiAspProGlyValaCysAsnTrpLys	377
Db	735	-----AAAGTCCCAACA-----	746
Oy	378	TyrTybPheIleValLeuAsnSerLeuAsnGlnAsnAlaLysProGlyGlyProGlnGln	397
Db	747	-----CTGTGAGTA-----	755
Oy	398	AlaGluLeuGlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProPro	417
Db	756	GAACAAAGTTCCACAAATTAAT-----	776
Oy	418	MetCisProGluLeuAsnLeuAspLeuGlnSerProThiLysLeuSerAlaSerGlyGluAsp	437
Db	777	-----GATTAATTCAAGACTCGAG-----TTGACATCAAGTTGTGGAA	812
Oy	438	SerThrIleProGlnAlaSerArgLysLeuAsnAlaValAsnArgSerMetThrGly--	456
Db	813	ATACTTTTCCAGACAAAGATATGTGTCCACACTGTTCACGTGAAGAAACCGGAAAC	872
Oy	457	---SerProArgSerSerSerGlnSerGlnSerHisSerProLeuLysMetHisProProLysCys	475
Db	873	TCACAGCCAACTGTGCTGTGAAGAAACACTCT-----ATGCTCT	911
Oy	476	ThrSerCysGlySerGlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyPro	495
Db	912	AATTAAGCCAGCGTCMAAGAGTCTTATAGAGCGGAG-----	947
Oy	496	ThrPheAlaGluGluMetGlyGlyThrGlnSerGlyLysTrpSerAspSerSerCysGluAsn	515
Db	948	AATCCCGGGAGAGCTGGATCAAGAGGTATTCAGAGCCCAAGCCA-----	992
Oy	516	GlyAlaPhePheCysAsnGlnCysAspCysArgPheSerGlnGluAlaSerLeuLysArg	535
Db	993	-----ATGTGTAACAATGTGGAAAGTGTTCAGAAAGCCAGACGTTTGAGAAAG	1043
Oy	536	His-----	536
Db	1044	CACATGAGAAATACATAAAGAGTCAAACTTAAGTCCACTTATGTGGAAAGCAATTT	1103
Oy	537	-----ThrLeuGlnThrHis-----SerAspLysProTyrLys	547
Db	1104	ACCCAAATGTAAACAGACTGTGAACCCCATGTAGAACTCATACAGGTGAGAAACCCATACAAA	1163
Oy	548	CysAspArgCysGlnAlaSerPheArgTyrLysGlyAsnLeuAlaSerHisLysThrVal	567
Db	1164	TGTGAATTGTGTGATAAAGATTGGTCTCAGAAATGTCAAGCTAAGTCTTCCATAGTCGCAAT	1223
Oy	568	HisThrGly--GlyLysProTyrArgCysAsnLysCysGlyAlaGlnPheAsnArgPro	586
Db	1224	CATCATGGGTGAAGAAAACCTTAATAATGTGATGATGATCACTTAACAGTTTGGCAACTCT	1283
Oy	587	AlaAsnLeuLysThrHisThrArgGluLeuHiserGlyGlyLysProTyrLysCysGluThr	606
Db	1284	AGCAATCTCCAAAGATTCAATCATGCAAGGAAGCATGTGAGAAAGCCATATGTCTGTGATAGG	1343
Oy	607	CysGlyAlaAspPheValGlnValAlaHisLeuArgAlaHisVal-----LeuIle	623
Db	1344	TGTGGACAGAAATTTGCTCAAGCCAGCACTGACCTATCATGTCTCCGTAAGGCATTACTG	1403
Oy	624	HisThrGlyGlyLysProTyrProCysGlyLysCysGlyLysThrArgPheArgHisLeuGln	643
Db	1404	-----GGAGAAAGCCTTATGTATGTGATGCTGTGGAAAGCCTTGTGCTGTCTAGT	1457
Oy	644	ThrLeuLysSerHisLysLeuArgGluLeuHisThrGlyGlyLysProTyrHisCysGlyLysCys	663
Db	1458	TCTCTTATCACTCACTTCTGAAAACATACAGAGTGAAGAAACCATACATATGTGTGATTTGT	1511
Oy	664	AsnLeuHisPheArgHisLysSerGlnLeuArgLeuHisLysLeuArgGlnLysHisGly	682
Db	1518	GGAAAAAGTTTATTTCTCTCAGAGAGACTCAAAACACTTTCCGTCCCATACAGGA	1574

## RESULT 14





Db 1407 CATGTACCGGACGAGGAGGCTACGAGACGGTGTCTTACGGGAGCAACTGTATGTGTGCAT 1466  
Qy 476 rSerCyGjlySerGlnSerProGln-----HSAIAGlUmeCyLeuH1stH 492  
Db 1467 TCCCTCGCCGCAAGAGGCTTCCCGACGCTGTAGACAGCTCAATGGCGACGTGAAGACTCACAC 1526  
Qy 492 rAlaGlyProThrPheAlaGluGluMetGly-----GluThr-----G1 505  
Db 1527 GAGAGAAAGACTTATCATCAAGAAAGAGGGGCTTACAGACAGGACAGTGGGGTCCCA 1586  
Qy 505 nSerGluTySerSerSerSerSerCyGjlyGlnGlyAlaPhePheCyAaGlnGluCyAaPry 525  
Db 1587 GAGAGAGGCGGACGAGCTGTACAGACCCAGTGGCGCTAC----- 1626  
Qy 525 aArgPheSerGluGluAlaSerLeuYarGhi1stHLeuGlnThrH1SerAryPr 545  
Db 1627 -----ACGAGCTGAGCCCGCGCC 1643  
Qy 545 oTyLyysCyAaPryCyGjlyAlaSerPheArgTyLyysGlyAaLeuAlaSerH1stH 565  
Db 1644 CTTCAGAGTTCGCTGTGCGAGAAAGACTTACAGAGACCCAGCAGCTGGCGAGACCA 1703  
Qy 565 stHrValH1stHrGlyGlyLeuPProTyArgCyAaGlnGlyAaGlnPheAaHr 585  
Db 1704 GAGAGACGACTGGCTGACAGCGGCTTCCCTCAACATCTGTGGCAAAATGTTCAAGCA 1763  
Qy 585 gProAlaLeuLeuLeuTh1stHrArgLeH1stHrGlyGlyLeuPProTyArgCyGj 605  
Db 1764 GCGCGGACCATGACGCGTGCATGCGAGACCATGCGGCTGAAAGCTTCCGCTGCA 1823  
Qy 605 uThrCyGjlyAlaArgPheValGlnValAlaH1stHrGlyAlaH1stHrGly 625  
Db 1824 TGAGTGTGGATGCGCTTCCAGCCGTCAGTACCCGCTCAGAGACATGGTGTGACATC 1883  
Qy 625 rGjlyGlyLeuPProTyArgCyGjlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 645  
Db 1884 GGGGAGAAACCTTACAGAGTGCAGCTGTGCGGGGAGCAAGTTCAACCAGAGCGCAACT 1943  
Qy 645 uLySerH1stHrLeuArgLeH1stHrGlyGly-----LysPro----- 657  
Db 1944 CATCAGCCACTGCGCATGACACCTTCCCTCTAGAACCAAAAGCAGCGGCGGCGC 2003  
Qy 658 -TyH1stHrCyGjlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 663  
Db 2004 CCATCATGCCAACCCTTGC 2022

RESULT 15  
US-10-120-988-145  
; Sequence 145, Application US/10120988  
; Patent No. 6919193  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Ren, Feiyun  
; APPLICANT: Wang, Dуннu  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6919193el Nucleic Acids and  
; FILE REFERENCE: Polypeptides  
; CURRENT APPLICATION NUMBER: US/10/120,988  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: 09/774,528  
; NUMBER OF SEQ ID NOS: 441  
; SOFTWARE: pc\_fl\_genes Version 2.0  
; SEQ ID NO 145  
; LENGTH: 2948  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (133)..(1980)

US-10-120-988-145  
Alignment Scores:  
Pred. No.: 3,448-28  
Score: 498.50  
Percent Similarity: 37.64  
Best Local Similarity: 25.24  
Query Match: 13.14  
DB: 3  
Gaps: 26

US-10-755-889-18 (1-706) x US-10-120-988-145 (1-2948)

Qy 9 IleglnPheThrArgH1stHrAlaSerAryAlaLeuLeuAaLeuAaHrGlySerArg 28  
Db 199 ATGAGAGCTGCCAGGACATCGAAGAGAGCTGCTGTGACAGCTGAACCAAGAGAGCAAG 258  
Qy 29 AaplleuThrAryAlaValIleValAlaSerAryGluGlnPheArgAlaH1stHr 48  
Db 259 GCGTTCCTGTGTGAGTGCATCATGTGTGAGAACTCCATCTTCCGGGCGCAAGAAC 318  
Qy 49 ValLeuMetAlaCySerGlyLeuPheTySerIlePheThrAryGlnLeuLeuCyAaHn 68  
Db 319 GTCTAGCCCGCAGC-----ACATCTATTTCAGTCCCTGCTGTGAC 363  
Qy 69 LeuSerValIleAaLeuAaPProGlu-----IleAaPProGluGlyPheCyA1leLeuLeu 87  
Db 364 GACAACTCATCACTGTGACACAGACATGTGCAGCTCCACAGTGTCCAGAGATCTTG 423  
Qy 88 AaplleuMetTyThrSerArgLeu-----AaLeuArgGluGlyAaH1stHrMet 103  
Db 424 GACTTCATCTACACAGGAGAGCTGTGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 483  
Qy 104 AlaValMetAlaThrAlaMetTyThrLeuGlnMetGlnH1stHrValIleAaPThrCyAaHr 123  
Db 484 ACCCTTCAGTCCGCGCAGTACCTTCCAGCTGCCAGCTGCCAGTGTGAGAGCTTCCGCGCC 543  
Qy 124 PheIleLeu-----AlaSerGluAlaGluMetValSerAlaIle 136  
Db 544 AAATCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 603  
Qy 137 LysPProArgGlyGluGluPheLeuAaSerAryMetLeuMetPProGlnAaplleuAla 156  
Db 604 CGGCCCCCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 662  
Qy 157 TyArgGlyArgGluValAlaGluAaLeuLeuPro----- 168  
Db 663 GCTGTGTGTGAGGCGCAGGAGGAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 722  
Qy 169 -----LeuArgSerAlaPProGly 174  
Db 723 AGACGATGAACCTTTCTGTGTGTGCTCTAACCAGAGTAGCGTGAAGGCTGTGGCGCGGCG 782  
Qy 175 CyGjlySerArgAlaPheAlaPProSerLeuTySerGlyLeuSer-ThrPProAlaAse 194  
Db 783 TGT-----CTGCCAGCTGCGCGGAGGCGGAGCTGTGGGAGGCTGCAGAG 827  
Qy 194 rTySerMetTySerH1stHrLeuPProValSerSerLeuLeuPheSerAryGluGluPheAr 214  
Db 828 CAGCAGCAACGAGAGCGGAGGCTGCGAGCAGAGAGCTGGGCTTGGACTTGCACAGAA 887  
Qy 214 GAAPValAryMetPProValAlaAaPProPhePProGlyAryAlaLeuPProCyAaPse 234  
Db 888 AAGCCAGCAGTGTGCG 941  
Qy 234 rAlaArgPProValPProGlyGluTySerArgPProThrLeuGluValSerPProAaValCy 254  
Db 942 AGCCAGCTGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1001  
Qy 254 stH1stHrAaH1stHrSer-----PProGlyThrH1stHrPProGluGlu 269  
Db 1002 CAACAGTGCCTTATTTAGCTGTGGGAGCAGCAGCAGTGAAGCCATGATGTGAAGG 1061  
Qy 269 aArgSerAryMetH1stHrSerValAlaGluGlyLeuPProAlaAlaPProSerAlaAr 289

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Db      1062 GGGCGAGACACCTGAGCTGCTGAG-----GGGCTGCTGGCGCA 1106
Qy      289 gaaAlaProTyrPheProCysAapLysAlaSerLysGluGluArgProSerSerg1 309
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Qy      309 uAapGluIleAlaLeuHisPheGluProProAsnAlaProLeuAsnArgLysGlyLeuVa 329
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Qy      329 lSerProGlnSerProGlnLysSerAapCysGlnProAsnSerProThrGluAlaCysSe 349
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Qy      349 rSerLysAsnAlaCysIleLeuGlnAlaSerGlySerProProAlaLysSerProThraS 369
Db      1242 GGACAGGGTTCCCAATGACATCTGCTAGTGG----- 1275
Qy      369 pProLysAlaCysAsnTrpLysLysTyrLysPheIleValLeuAsnSerLeuAsnGlnAs 389
Db      1275 ----- 1275
Qy      389 nAlaLysProGlyGlyProGluGlnAlaGluLeuGlyArgLeuSerProArgAlaTyrTh 409
Db      1276 -GCTGGCTTAGCGGCGCC-----TATGG 1298
Qy      409 rAlaProProAlaCysGlnProMetGluProGluAsnLeuAapLeuGlnSerProTh 429
Db      1299 GGAGCCCCC-----TACCTTCGCAAGAGAGAGAGAG- 1332
Qy      429 rLysLeuSerAlaSerGlyLysAapSerThrIleProGlnAlaSerArgLeuAsnAl 449
Db      1333 -----AACGCCAAGATGCAAGTGAAGACAGTGC----- 1362
Qy      449 eValAsnArgSerMetThrGlySerProArgSerSerSerGluSerHisSerProLeuTy 469
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Qy      469 rMetHisProProLys-----CysTh 476
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Qy      476 rSerCysGlySerGlnSerProGln-----HisAlaGluMetCysLysuHisTh 492
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Qy      492 rAlaGlyProThrPheAlaGluGluMetGly-----GluThr-----G1 505
Db      1527 GGAGGAGAGAGCTGTCATCAAGAAAGAGGGGCGCTACGAGACAGTGGGGGTGCCGA 1586
Qy      505 nSerGluTyrSerAapSerSerCysGluAsnGlyAlaPhePheCysAapGluCysAapCy 525
Db      1587 GGAGAGGGCCGAGAGCTGTGACGACCCAGTGGCGCTTAC----- 1626
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Qy      545 oTyrLysCysAapArgCysGlnAlaSerPheArgTyrLysGlyAsnLeuAlaSerHisLy 565
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Qy      565 sThrValHisThrGlyLysLysProTyrArgCysAsnIleCysGlyAlaGlnPheAsnAr 585
Db      1704 GAAGAGGACTGCTGACAGGGCTTCCCTCGCAACATCTGGGCAAAATGTTACGCA 1763
Qy      585 gProAlaAsnLeuLysThrHisThrArgIleHisSerGlyLysLysProTyrLysCysG1 605
Db      1764 GCGCGGACACATGAGCGGTCAATGCGAGGACCTGGGCGCTGAGCCCTTGCGCTGCGA 1823
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Qy      645 uLysSerHisLeuArgIleHisThrGlyLys-----LysPro----- 657
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GenCore version 5.1.7  
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Run on: March 2, 2006, 01:57:00 ; Search time 1444 Seconds  
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4043.062 Million cell updates/sec

Title: US-10-755-889-18

Perfect score: 3793

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3793	100.0	3536	US-09-880-107-3271	Sequence 3271, Ap
2	3793	100.0	3536	US-10-776-827-90	Sequence 90, Appl
3	3793	100.0	3536	US-10-755-889-17	Sequence 17, Appl
4	3793	100.0	3536	US-10-755-889-65	Sequence 65, Appl
5	3777	99.6	4506	US-10-252-157-169	Sequence 169, App
6	3763	99.2	3720	US-09-107-058-1	Sequence 1, Appl
7	3763	99.2	3720	US-09-761-117-1	Sequence 1, Appl

8	1155	30.5	3676	US-10-295-027-15	Sequence 15, Appl
9	1155	30.5	3676	US-10-211-462-23	Sequence 23, Appl
10	1122.5	29.6	1749	US-09-815-379-3	Sequence 3, Appl
11	630	16.6	2741	US-10-974-440-92	Sequence 92, Appl
12	621.5	16.4	2769	US-10-037-270-309	Sequence 309, App
13	621.5	16.4	2769	US-10-117-722-309	Sequence 309, App
14	621.5	16.4	2769	US-10-122-851-309	Sequence 109, App
15	567	14.9	3451	US-10-486-977-45	Sequence 45, Appl
16	540	14.2	2289	US-10-477-646-22	Sequence 22, Appl
17	524.5	13.8	2826	US-10-221-625-117	Sequence 117, App
18	521	13.7	4950	US-10-034-934-13	Sequence 13, Appl
19	521	13.7	6190	US-10-676-2488-24	Sequence 24, Appl
20	514.5	13.6	2887	US-10-108-2604-859	Sequence 859, App
21	509.5	13.4	3349	US-10-108-2604-65	Sequence 65, Appl
22	508	13.4	2407	US-10-357-930-21308	Sequence 21308, A
23	508	13.4	2407	US-10-357-930-23642	Sequence 23642, A
24	508	13.4	2407	US-10-357-930-27150	Sequence 27150, A
25	508	13.4	2407	US-10-357-930-29533	Sequence 29533, A
26	504	13.3	2393	US-10-296-115-577	Sequence 577, App
27	503	13.3	3052	US-10-104-047-959	Sequence 959, App
28	501	13.2	2170	US-10-504-173-112	Sequence 112, App
29	501	13.2	2197	US-10-172-118-1228	Sequence 1228, App
30	501	13.2	2197	US-10-342-887-1228	Sequence 1228, App
31	501	13.2	2197	US-10-956-157-1519	Sequence 1519, App
32	501	13.2	2197	US-10-756-149-169	Sequence 169, App
33	500	13.2	2920	US-10-037-270-1084	Sequence 1084, App
34	500	13.2	2920	US-10-117-722-1084	Sequence 1084, App
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37	498.5	13.1	2948	US-10-120-988-145	Sequence 145, App
38	498	13.1	3434	US-10-450-763-9676	Sequence 9676, App
39	497.5	13.1	4029	US-10-450-763-1717	Sequence 1717, App
40	495.5	13.1	6793	US-10-723-860-1612	Sequence 1612, App
41	495.5	13.1	6994	US-10-723-860-6021	Sequence 6021, App
42	495	13.1	2330	US-10-305-720-1054	Sequence 1054, App
43	494.5	13.0	1947	US-10-136-728-57	Sequence 57, Appl
44	494.5	13.0	3058	US-10-887-553A-569	Sequence 569, App
45	493.5	13.0	1794	US-10-029-386-25094	Sequence 25094, A

#### ALIGNMENTS

RESULT 1  
US-09-880-107-3271  
Sequence 3271, Application US/09880107  
Patent No. US20020142981A1  
GENERAL INFORMATION:  
APPLICANT: Horne, Darci T.  
APPLICANT: Schert, Uwe  
APPLICANT: Joseph G.  
TITLE OF INVENTION: Gene Logic, Inc.  
FILE REFERENCE: 44921-5028-WO  
CURRENT APPLICATION NUMBER: US/09/880,107  
CURRENT FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: US 60/211,379  
PRIOR FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: US 60/237,054  
PRIOR FILING DATE: 2000-10-02  
NUMBER OF SEQ ID NOS: 3950  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 3271  
LENGTH: 3536  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURES:  
OTHER INFORMATION: Genbank Accession No. US20020142981A1 U00115  
US-09-880-107-3271  
Alignment Scores:  
Pred. No.: 0  
Score: 3793.00  
Percent Similarity: 100.0%  
Length: 3536  
Matches: 706  
Conservative: 0

Best Local Similarity:	100.0%	Mismatches:	0
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QY	1	MetAlaSerProAlaAspSerCysIleGlnPheThrArgHisAlaSerAspValLeuLeu	20
DB	328	ATGGCTCGCGGCTGACAGCTGATACAGTTCACCGCATGCCAGTATGTTCTTCTC	387
QY	21	AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValIleValValSerArg	40
DB	388	AACCTTAATGCTCTCCGAGTCGAGACATCTTGACTGATGTTGTCAATTGTGAGACCGGT	447
QY	41	GlulGlnPheArgHisIleValThrValLeuMetAlaCysSerGlyLeuPheTyrSerIle	60
DB	448	GAGCAGATTGAGACCCATAAAGGCTTCATGCGCTGACGAGCGCTGTTCAATACATC	507
QY	61	PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro	80
DB	508	TTTACAGACCAAGTTGAATGCCAATTAAGTGTATCATCTAGATCTGAGATCAACCT	567
QY	81	GlulGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly	100
DB	568	GAGGATTCCTGCAATCCTCGACTCATATGATACATCTCGCTCAATTTGCGGAGAGGC	627
QY	101	AsnIleMetAlaValMetAlaThrAlaMetTyrIleGluMetGluHisValValAspThr	120
DB	628	AACATCATGGCTGTGAGGCGCACGGCTATGTACCTGACAGTAGAGCATGTTGTGACACT	687
QY	121	CysArgGlyPheIleValSerGluValGluMetAlaSerAlaIleLysProProArg	140
DB	688	TGCGGAAAGTTTATTAAGCCAGTAGAGCAGAGATGTTTCTGCCATCAAGCTCTCTCG	747
QY	141	GlulGlnPheLeuAsnSerArgMetLeuMetProGluAspIleMetAlaTyrArgGlyArg	160
DB	748	GAAAGATTCTCAACAGCCGAGATGCTGATGCCCAAGACATCATGGCTCATCGGGATCGT	807
QY	161	GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe	180
DB	808	GAGGTGTGTGAGAACCACTGCGCATGAGAGCGCCCTGGGTGTGAGACCAAGCTT	867
QY	181	AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis	200
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QY	201	LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspValArgMetProVal	220
DB	928	CTCCCTGTGACAGCCTCTCTCTCCGATGAGGAGTTTCGGGATGTCGGATGCCGTGTG	987
QY	221	AlaAsnProPheProLysGluArgAlaLeuProCysAspSerAlaArgProValProGly	240
DB	988	GCCAAACCCCTTCCCAAGAGCGGCGCATCCCATGTATGTGTCAGACCAATATCTATTC	1047
QY	241	GluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyrSer	260
DB	1048	GAGTACGCGCGCGCATTTGAGAGTGTCCCCCAATGTGTGCCACAGCAATATCTATTC	1107
QY	261	ProLysGluThrIleProGluGluValArgSerAspMetHisTyrSerValAlaGluGly	280
DB	1108	CCCAAGGAAACATCCAGAAAGGCGACGAAGTGATGTGACATCACTGTGGCTGAGGGC	1167
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DB	1168	CTCAAACTGCTGCTCCCTCAGCCCGAAATGCCCTTACTTCTGTGCAAGGCGCAGC	1227
QY	301	LysGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAsn	320
DB	1228	AAAGAAAGAGAGACCTCTCTCGAAGATGAGATTCCTCTGACATTCGAGCCCCCAAT	1287
QY	321	AlaProLeuAsnArgLysGlyLeuValSerProGlnSerProGlnLysSerAspCysGln	340
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QY	341	ProAsnSerProThrGluAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSerGly	360
DB	1348	CCCAACTGCGCCACAGAGGCTCGAGCAGTAGAATGCTGATCTCCAGGCTTCTGGC	1407
QY	361	SerProProAlaLysSerProThrAspProLysAlaCysAsnTyrLysTyrLysPhe	380
DB	1408	TCCCTCCAGCCAAAGGCCCTGATGCCCAAGCTCCATCTGAGAAATATCAAGATTC	1467
QY	381	IleValIleAsnSerLeuAsnGlnAsnAlaLysProGlyGlyProGluGlnAlaGluLeu	400
DB	1468	ATGTTGCTCAACAGCTTCAACAGATGCCAAACAGAGGAGCTTGAGCAGGCTGAGCTG	1527
QY	401	GlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProPheMetGluPro	420
DB	1528	GCGCCGCTTCCCAAGAGCTTACACGGCCCACTGCTGTCACACCACTGAGAGCT	1587
QY	421	GluAsnLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIle	440
DB	1588	GAGAACCTTGACCTCCAGTCCCAACCAAGCTGAGTCCAGCGGAGGAGACTCCACATTC	1647
QY	441	ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer	460
DB	1648	CCACAGCCAGCGGCTCAATATCAATCGTTACAGATCATAGCAGGCTCTCCCGCAC	1707
QY	461	SerSerGluSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer	480
DB	1708	AGCAGCGAGGACCATCAACCATCTACATGACCCCGAATGACAGTCCGCGGCTCT	1767
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DB	1828	ATGGAGAGAACCCAGCTGAGTACTCAGATTTAGCTGTGAAACGGGAGCTTCTTCTGC	1887
QY	521	AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr	540
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QY	541	HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn	560
DB	1948	CACAGTGAACAACCTTACAAAGTGTACCGTCCAGGCTCTCCCTCCGCTTACAAAGGCAAC	2007
QY	561	LeuAlaSerHisIleThrValHisThrGlyGlyLysProTyrArgCysAsnIleCysGly	580
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DB	2068	GCCCATTTCAACCGGCACACCACTGAAACCCACATCTGAAATCACTTGGAGAGAG	2127
QY	601	ProTyrLysCysGluThrCysGlyAlaArgPheValGlnValAlaHisLeuArgAlaHis	620
DB	2128	CCCTTAACAATGGAAACCTGCGGAGCAGATTTGTACAGTGGCCCACTCCGTGCCAT	2187
QY	621	ValLeuIleHisThrGlyGlyLysProTyrProCysGluIleCysGlyTyrThrArgPheArg	640
DB	2188	GTGCTTATCACACTGTGTAGAGAGCCCTATCCCTGTGAATCTGTGGCACCGGTTCCGG	2247
QY	641	HisLeuGlnThrLeuLysSerHisLeuArgIleHisThrGlyGlyLysProTyrHisCys	660
DB	2248	CACCTTCAACCTTGAAAGGCCACTCGAATTCACACAGAGAGAAACCTTACATTTGT	2307
QY	661	GluLysCysAsnLeuHisPheArgHisIleSerGlnLeuArgLeuHisLeuArgGlnLys	680
DB	2308	GAGAAATGTACCTGTGATTTCCGTCAAAAGCAGCTGCACTTCACTTGCGCCAGAG	2367
QY	681	HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro	700
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QY 701 GluLeuProIyalaCys 706  
DB 2428 GAGCTCCCAAGCTGC 2445

## RESULT 2

US-10-776-827-90  
Sequence 90, Application US/10776827  
Publication No. US20040132086A1  
GENERAL INFORMATION:  
APPLICANT: Horvitz, Kathryn  
APPLICANT: Richter, Jennifer  
TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Related  
TITLE OF INVENTION: Inhereco  
FILE REFERENCE: 2848-39  
CURRENT APPLICATION NUMBER: US/10/776,827  
CURRENT FILING DATE: 2004-02-10  
PRIOR APPLICATION NUMBER: US/09/814,915  
PRIOR FILING DATE: 2002-03-21  
PRIOR APPLICATION NUMBER: 60/214,870  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 90  
LENGTH: 3536  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-776-827-90

## Alignment Scores:

Pred. No.: 0 Length: 3536  
Score: 3793.00 Matches: 706  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 7 Gaps: 0

US-10-755-889-18 (1-706) x US-10-776-827-90 (1-3536)

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DB 388 AACCTTATGCTGCTCCGAGAGTCAAGACATCTTGACTGATGTTGTCATGTTGTAGCGGT 447  
QY 41 GluGlnPheArgAlaHisIlyThrValIleuMetAlaCysSerGlyLeuPheTyrSerIle 60  
DB 448 GAGCAGTTTGAAGCCATAAAACGCTCTCATGCTGCAAGTGGCTGTTCTTATAGCATC 507  
QY 61 PheThrAaP1IleuLeuArgCysAsnLeuSerValIleAsnLeuAaPProGluIleAsnPro 80  
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QY 81 GluGlyPheCysIleLeuLeuAaPPhMetTyrThrSerArgLeuAsnLeuArgGluGly 100  
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QY 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValIaAspThr 120  
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QY 121 CysArgIysPheIleValIaSerGluAgluMetValSerAlaIleIlePProProArg 140  
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QY 141 GluGlnPheLeuAsnSerArgMetLeuMetProGlnAaP1IleMetAlaTyrArgGlyArg 160  
DB 748 GAAAGGTTCTCAACAGCCGAGTGTGATGCCCCAAGACATCATGCTTATCGGGGTCT 807  
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QY 201 LeuProValSerSerLeuLeuPheSerAaP1GluPheArgAaPValIaArgMetProVal 220  
DB 928 CTCCCTGTAGCAGCTCTCTTCTCCAGTAGAGATTTCCGGGATGTCGGAGATGCTGTG 987  
QY 221 AlaAsnProPheProIyGluArgAlaLeuProCysAaP1IleAaPProValIleProGly 240  
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QY 241 GluTyrSerArgProThrLeuGluValIleSerProAsnValCysHisSerAnIleTyrSer 260  
DB 1048 GAGTACAGCGCGGCGGCTTGTGAGGTGTCCCAATGTGTGACAGCAATATCTTATTC 1107  
QY 261 ProIyGluThrIleProGluGluAlaIySerAaP1MetHisTyrSerValIaGluGly 280  
DB 1108 CCCAAGAAACATCCCAAGAGGCAAGAGATATGCACTACAGTGTGCTGAGGGC 1167  
QY 281 LeuIySProAlaAlaProSerAlaArgAaP1AaProTyrPheProCysAaP1IleAaSer 300  
DB 1168 CTCAAACCTGTGCTCCCTCAGCGCCGAAATGCCCCCTACTTCCCTGTGACAGAGCGCAGC 1227  
QY 301 IySGLuGluGluArgProSerSerGlyAaP1IleAlaIleuHisPheGluProProAsn 320  
DB 1228 AAGAAAGAAAGAGAGCCCTCTCGAAGATGATGATTCCTGCAATTCAGAGCCCCCAAT 1287  
QY 321 AlaProLeuAnkArgIySGLuValIleSerProGlnIySerProGlnIySeraP1CysGln 340  
DB 1288 GCAACCTTGAACCGAAGGCTGTGTGTTAGTCCACAGAGCCCAAGAAATGTGACTGCAAG 1347  
QY 341 ProAsnSerProThrGluAlaCysSerSerIySAsnAlaCysIleLeuGlnAlaSerGly 360  
DB 1348 CCCAATCGGCCCAAGAGGCTGACAGATGATGATGCTGCACTCTCCAGGCTTCTGCGC 1407  
QY 361 SerProProAlaIySeraP1IleuValIleSerProGlnIySeraP1IleuValIleSerPhe 380  
DB 1408 TCCCTTCCAGCAGAGCCCAAGCTGACCCCAAGAGCTGCAATCTGAAAGAAATCAAGATTC 1467  
QY 381 IleValIleuAnkSerLeuAnkIleuAnkAlaIySeraP1IleuValIleSerPhe 400  
DB 1468 ATGTGTCAACAGCTTCAACAGATGCAAGATGCAAGAGGAGGCTGAGAGGCTGAGCTG 1527  
QY 401 GlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProPheMetGluPro 420  
DB 1528 GCGCGCTTCCCAAGAGCTGACAGGCTGACAGGCTGCTGCGCAGCAACCATGAGACT 1587  
QY 421 GluAsnLeuAaPLeuGlnSerProThrIySLeuSerAlaSerGlyIleuAaP1Ile 440  
DB 1588 GAGAACCTTGAAGCTTCCAGTCCCAACCAAGCTGATGCTGAGGAGGAGCTCCACCATC 1647  
QY 441 ProGlnAlaSerArgLeuAnkIleuValIleAsnArgSerMetThrGlySerProArgSer 460  
DB 1648 CCACAAACCGAGCGGCTCAATTAATGTGTAACAGGTCAAGAGGCTCTCCCGGAGC 1707  
QY 461 SerSerGluSerHisSerProLeuTyrMetHisProProIySGLuSerCysTyrSerGlySer 480  
DB 1708 AGCAGGAGAGCACTACCACTCTACATGCAACCCCGAAGTGCAGTCTGAGGCTCT 1767  
QY 481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500  
DB 1768 CAGTCCCAAGAGATGAGAGATGTGCTCCACAGCCCTGCGCCCAAGTTCGTGAGAGAG 1827  
QY 501 MetGlyIleuThrGlnSerGlyTyrSerAaP1IleuAnkIleuValIlePhePheCys 520  
DB 1828 ATGGAGAGAGCAAGTGTGATGATCTGATCTGATGATGAGAGGAGGCTCTTCTTCTG 1887  
QY 521 AsnGluCysAaP1CysArgPheSerGluGluAlaSerLeuIySArgHisThrLeuGlnThr 540  
DB 1888 AATGATGTATCTGCGCTTCTCTGAGAGAGGCTCACTCAAGAGGACACAGCTGCAAGC 1947

Qy	541	HisserAspLysProTyrLysCysAspArgCysGlnAspPheArgTyrLysGln	560
Db	1948	CACAGTACAAACCTTACAAAGTGTGACCGCTCCAGAGCTCTTCGGTACAAAGGAC	2007
Qy	561	LeuAlaSerHisLysLysThrValHisThrGlyGlyLysProTyrArgCysAsnIleCysGly	580
Db	2008	CTCCGCGAGCCCAAGACCGCTCCATACCGGTGAGAAACCTTCTCGTGGACATCTGTGGG	2067
Qy	581	AlaGlnPheAsnArgProAlaAsnLysThrHisThrArgIleHisSerGlyGlyLys	600
Db	2068	GCCCAAGTTCAACCGGCGACGCCACCTGTAACCAACCACTCGAATTCACTCTGGAGAGAG	2127
Qy	601	ProTyrLysCysGlyThrCysGlyAlaArgPheValGlnValIleHisLysArgAlaHis	620
Db	2128	CCCTAACAAATCGGAAACCTGGCGAGCCAGATTGTGACAGGTGGGCCACCTCCGGCCCAT	2187
Qy	621	ValIleuIleHisThrGlyGlyLysProTyrProCysGlnIleCysGlyThrArgPheArg	640
Db	2188	GTGCTTATCCACACTGTGTGAGAGGCCCTTATCCCTGTGAAATCTGTGGACCCCGTTCCGG	2247
Qy	641	HisLysGlnThrLysLysSerHisLysArgIleHisThrGlyGlyLysProTyrHisCys	660
Db	2248	CACCTTCAGACTCTGAAAGAGCCACCTTGCGAATCCACAGAGAGAGAACTTACCATTTGT	2307
Qy	661	GlyLysCysAsnLysHisPheArgHisLysSerGlnLysArgLeuHisLysArgGlyLys	680
Db	2308	GAGAAAGTATACCTGCATTTCCGTACAAAGCCAGCTGCACATTCACCTTGCGCGAGAG	2367
Qy	681	HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro	700
Db	2368	CATGCGCGCATACCAACCAACCAAGGTGCAATACCGGTGTAGCCACATGACCTGCTCCG	2427
Qy	701	GlyLeuProLysAlaCys	706
Db	2428	GAGCTCCCAAGGCTGC	2445

### RESULT 3

```

US-10-755-889-17
; Sequence 17, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 17
; LENGTH: 3536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-17

```

**Alignment Scores:**

Pred. No.:	0	3536
Length:	706	
Scores:	3793.00	
Percent Similarity:	100.0%	Conservative: 0
Best Local Similarity:	100.0%	Mismatches: 0
Query Match:	100.0%	Indels: 0
DB:	7	Gaps: 0

US-10-755-889-18 (1-706) x US-10-755-889-17 (1-3536)

QY 1 MetalSerProAlaaspSerCysIleGlnpHeThrtrgHisIaSerAspValIleuLeu 20  
Db 328 ATGGCCCTCGCCGCTGACAGCTGTATCCAGTTCACCCGCCATCCACAGATGATGTTCTTCTC 387

QY	21	AsnLeuSenrArgLeuAGSSerArgAspIleLeuThrAspValValIleValIleSerArg	40
Db	388	AACTTAATGCTCTCCGAGTCCAGACATCTTGACTATGTTGCACTTGTGACCGCT	447
QY	41	GlulInPheArgAlaHisIleThrValIleMetAlaCysSerGlyLeuPheTyrSerIle	60
Db	448	GAGCAAGTTTAGAGCCCATPAAACGGCTCCTCATGGCTCGACATGGCCGTGTTCTATAGCATC	507
QY	61	PheThrAspGlnLeuLeuGlyGAsnLeuSerValIleAsnLeuAspProGluIleAsnPro	80
Db	508	TTTACAGCCAGTTGAATGCAATGCACTTAAGTGTATCATCTAGTACTCGAGATCAACCT	567
QY	81	GlulGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly	100
Db	568	GAGGAGATTCTGCATCTCTCTGACTTATGTACATCTCGCTCAATTTGGGAGAGGC	627
QY	101	AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValAspThr	120
Db	628	AAACTCATGGCTGTGATGGCCACGGCTATAGTACTGCAGATGAGCATGTTGTGACACT	687
QY	121	CysArgIysPheIleIleValAspSerGluAlaGluMetValSerAlaIleIleValProProArg	140
Db	688	TGCCGGAAGTTATTAAAGCCAGCAAGCAAGATGATTTCTGCATCAAGCCCTCCGCT	747
QY	141	GlulGluPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyrArgGlyArg	160
Db	748	GAAAGATCTCTCAACAGCCGAGTCTGATGCCCCAAGACATCATGGCTTATCGGAGGCTGT	807
QY	161	GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe	180
Db	808	GAGGTGGTGGAGAACACCTGCCACTGAGAGCGCCCTGGGTGTGAGAGCAGACCTT	867
QY	181	AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis	200
Db	868	GCCCCAGCCGTGACAGTGGCTCTGCCACACCGGACGCTTTTTCATGTACATGACGCAC	927
QY	201	LeuProValIleSerSerLeuLeuPheSerAspGluGluPheArgAspValArgMetProVal	220
Db	928	CTCCTGTACACAGCTCTCTCTCTCCATAGAGAGTTCCGAGATGTCGGATGCTGTG	987
QY	221	AlaAsnProPheProTyrGluArgAlaLeuProCysAspSerAlaArgProValProGly	240
Db	988	GCCAAACCCCTTCCCAAGAGAGCGGCACTCCCATGTGATATGCGCAGGCCAGTCCCTGGT	1047
QY	241	GluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyrSer	260
Db	1048	GAGTACACCGGCGCACTTTGAGAGGTGCCCCCAATGTGTGCCACAGCAATATCATTTCA	1107
QY	261	ProIysGluThrIleProGluGluValArgSerAspMetHisTyrSerValAlaGluGly	280
Db	1108	CCCAAGGAACATCTCCAGAAAGGCAAGAAGTATAGCATCAAGTGTGGCTGAGAGGC	1167
QY	281	LeuIysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspIleAspSer	300
Db	1168	CTCAAACTGCTGCCCCCTCAGCCCGAAATGCCCTTACTTCTGTGTGACAAGCCAGC	1227
QY	301	LysGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAsn	320
Db	1228	AAAGAAAGAGAGACCTCTCCGGAAGATGAGATTGCCCTGCAATTTGAGACCCCCCAAT	1287
QY	321	AlaProLeuAsnArgIysGlyLeuValSerProGlnSerProGlnIlySerAspCysGln	340
Db	1288	GCAACCCCTGAACCGGAGAGGTCTGGTTGTCCACAGAGACCCCCAGAAATCTGACTGCCAG	1347
QY	341	ProAsnSerProThrGluAlaCysSerSerIysAsnAlaCysIleLeuGlnAlaSerGly	360
Db	1348	CCAAACTGCCCCACAGAGGCTTGCAGCATAGAAATGCTGTGACTTCTCAAGCTTCTGGC	1407
QY	361	SerProProAlaIlySerSerProThrAspProIlyAsnAlaCysAsnTyrIlySerIysPhe	380
Db	1408	TCCCTCCAGCCAAAGGCCCACTGATCCCAAGGCTTCACTGGAAGAAATACAAAGTTCC	1467
QY	381	IleValIleuAsnSerLeuAsnGlnAsnAlaIlySerProGlyGlyProGluGlnAlaGluLeu	400



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Db      1468 ATCTGTCTCAACACCTTCAACCAAGATCCAAACAGGGGGGCTTGAGAGGCTGAGCTG 1527
Qy      401 G1YArgLeuSerProAlaAlaYrThrAlaProProAlaCysGlnProProMetGluPro 420
Db      1528 GGGCGCTTTCCTCCACAGGCTTACACGGCCCACTGCTGCGACCAACCCATGAGACCT 1587
Qy      421 GluAlaLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIle 440
Db      1588 GAGAACTTTCAGCTCCAGTCCCAACCAAGCTGAGTGCAGCGGGGAGGAGATTCACCAATC 1647
Qy      441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrLysSerProArgSer 460
Db      1648 CCACAGCGCAGCGGCTCAATAACATGCTTAACAGGTCTCAATGAGCGGCTCTCCCGAGAC 1707
Qy      461 SerSerGlnSerHisSerProLeuThrMetHisProProLysCysThrSerCysGlySer 480
Db      1708 AGCAGCGAGAGCCACTCAACCTTACATGCAACCCCGAAGTGCAGCTCTGCGGCTCT 1767
Qy      481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500
Db      1768 CAGTCCCGCAGCATGAGAGATGTCCTCCACACCGCTGGCCCCAGCTTCGCTGAGAGAG 1827
Qy      501 MetGlyGlnThrGlnSerGlnThrSerAspSerSerCysGluAsnGlyAlaPhePheCys 520
Db      1828 ATGGAGAGAGACCCAGTCTGAGTACTGAGATTCTAGCTGTGAGAACGGGGCTTCTTCTGC 1887
Qy      521 AsnGluCysAspCysArgPheSerGlnGluAlaSerLeuLysArgHisThrLeuGlnThr 540
Db      1888 AATAGATGTAGCTGCGCTTCTTGAGAGGCTCTCACTCAAGAGGACACCTCTGAGACC 1947
Qy      541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560
Db      1948 CACAGTACAAACCTTACAGTGTGACCGCTGACAGGCTCTCCGCTTCCGCTTCAAGAGG 2007
Qy      561 LeuAlaSerHisLysThrValHisThrGlyGluLysProTyrArgCysAsnIleCysGly 580
Db      2008 CTCCGACAGCCCAAGACCGTCCATACCGGTGAGAAACCTTATCGTTGCAACATCTGTGG 2067
Qy      581 AlaGlnPheAsnArgProAlaAsnLeuSerThrHisThrArgIleHisSerGlyGluLys 600
Db      2068 GCCCAGTTCAACCGGCGCCAGCCCACTGAAACCCCACTCGAATTCATCTTGAGAGAGAG 2127
Qy      601 ProTyrLysCysGluThrCysGlyAlaAlaArgPheValGlnValAlaHisLeuArgAlaHis 620
Db      2128 CCTTACAAATGCGAAACCTGGAGAGCCAGATTTTGTACAGGTGGCCCACTCGTCCCAT 2187
Qy      621 ValLeuIleHisThrGlyGluLysProTyrProCysGluIleCysGlyThrArgPheArg 640
Db      2188 GTGCTTATCCACACTGTGTGAGAAAGCCCTATCCCTGTGAATCTGTGGACCCGTTTCCGG 2247
Qy      641 HisLeuGlnThrLeuLysSerHisLeuArgIleHisThrGlyGluLysProTyrHisCys 660
Db      2248 CACCTTCAGACTTGAGAGAGCCACTGGAAATCCACAGAGAGAGAAACCTTACCATTTGT 2307
Qy      661 GluLysCysAsnLeuHisPheArgHisLysSerGlnLeuArgLeuHisLeuArgGlnLys 680
Db      2308 GAGAAAGTTAACTGCACTTTCGCTGCAAAAGCCAGCTGCACTTCACTTGGGCCAAGAG 2367
Qy      681 HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700
Db      2368 CATGGCGCCATCACCAACCAAGGTGCAATACCGGTGTCAGCCACTGACCTGCTCCG 2427
Qy      701 GluLeuProLysAlaCys 706
Db      2428 GAGCTCCCAAGCCTGC 2445

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RESULT 4  
 US-10-755-889-65  
 ; Sequence 65, Application US/10755889  
 ; Publication No. US20040171823A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company

```

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 3536
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-755-889-65

Alignment Scores:
Pred. No.: 0 Length: 3536
Score: 3793.00 Matches: 706
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-755-889-18 (1-706) x US-10-755-889-65 (1-3536)

Qy      1 MetAlaSerProAlaAspSerCysIleGlnPheThrArgHisAlaSerAspValLeuLeu 20
Db      328 ATGGCTCGCGCGGTGACAGCTGATTCAGTTCACCCGACATGCAAGTGAATGTTCTTCTC 387
Qy      21 AsnLeuAsnArgLeuAlaGSerArgAspIleLeuThrAspValIleValIleValSerArg 40
Db      388 AACCTTATGCTCTCCGAGATCAGAGATCTTGAATGTCATGTGTCATGTGTGAGCGGT 447
Qy      41 GluGlnPheArgAlaHisLysThrValLeuMetAlaCysSerGlyLeuPheYrSerIle 60
Db      448 GAGCATGTTAGAGCCCATTAACCGTCTCTAGTGCCTGAGAGTGGCCGTCTTATAGCATC 507
Qy      61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80
Db      508 TTTTACAGACCGTTGAATGCAACCTTATGATGATCATCATGATCTGAGATCAACCTCT 567
Qy      81 GluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100
Db      568 GAGGATTCGACATCCCTCGACTTCATGATACATCTGGCTCAATTGGCGAGAGGCG 627
Qy      101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValValAspThr 120
Db      628 AACATCATGGCTGTGATGGCCACGGCTATGATCTGAGATGAGCATGTTGTGACACT 687
Qy      121 CysArgLysPheIleLysAlaSerGluAlaGluMetValSerAlaIleLysProProArg 140
Db      688 TGCCGGAAGTTATTAAGGCAAGTGAAGAGAGATGTTCTGCAATCAAGCCTCTCGT 747
Qy      141 GluGlnPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaIyrArgGlyArg 160
Db      748 GAAAGATTCTCAACACCGGATGCTGATGCCCCAAGCAATCATGAGGCTTAAGGGGTCTG 807
Qy      161 GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGlnSerArgAlaPhe 180
Db      808 GAGGTGTGTGAGAAACCTGCACTGAGAGAGCCCTTGAGTGTGAGAGAGAGAGCTTT 867
Qy      181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200
Db      868 GCCCGCAGCGGTACAGTGGCTGTCCACACCGCAGCCTCTTATTCATATACAGCAC 927
Qy      201 LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspValArgMetProVal 220
Db      928 CTCCCTGACAGACCTCTCTCTTCTCGATGAGAGATTTGCGAGTGTCCGATCCCTGTG 987
Qy      221 AlaAsnProPheProLysGluArgAlaLeuProCysAspSerAlaArgProValProGly 240

```

Db GCCAACCCCTTCCCAAGAGCGGCACTCCATGATGATGTCAGGCGAGCTCCGTG 1047  
 Qy 241 GlnTyrSerProThrLeuGlnValSerProSerValCysHisSerAsnIleTyrSer 260  
 Db 1048 GAGTACAGCGCGCGAGCTTGGAGGTGTCCCAAGTGTGGCCAGCAATATCTATCA 1107  
 Qy 261 ProLysGlnThrIleProGlnGlnValArgSerAspMetHisTyrSerValAlaGln 280  
 Db 1108 CCCAAGGAACATCTCCAGAAAGGCGACGAAATGATGACATCAAGTGTGGTGAAGG 1167  
 Qy 281 LeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLysAlaSer 300  
 Db 1168 CTCAAACTGTCTGCTCCCTCAGCGCCGAATGCCCCCTCACTTCCCTGTGCAAGGCGCAG 1227  
 Qy 301 LysGlnGlnGlnArgProSerSerGlnValArgLysAlaIleuHisPheGlnProProAn 320  
 Db 1228 AAGAAAGAGAGAGAGCTCTCGAAGATGAAATGGCTGTGATTTCAAGCCCCCAAT 1287  
 Qy 321 AlaProLeuAsnArgLysGlnLeuValSerProGlnSerProGlnLysSerAspCysGln 340  
 Db 1288 GCACCCCTGAACCGGAAGGCTGTGTTAGTCCAGAGCCCCCGAATCTGATGCTCCAG 1347  
 Qy 341 ProAsnSerProThrGlnAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSerGln 360  
 Db 1348 CCCAACTCGCCCAAGAGCGCTGAGAGATGATGATCTGCAATCTCCAGGCTTCTGGC 1407  
 Qy 361 SerProProAlaLysSerProThrAspProLysAlaCysAsnTrpLysLysPhe 380  
 Db 1408 TCCCTCTCAGCCAGAGCGCCCTGAGAGCTCCCAAGCTCGCAAGTCAAGATTC 1467  
 Qy 381 IleValLeuAsnSerLeuAsnGlnAsnAlaLysProGlnValProGlnGlnAlaGlnLeu 400  
 Db 1468 ATCTGTCTCAACAGCTCCACCAAGATGCCAAACAGAGGCGGCTGAGAGGCTGAGCTG 1527  
 Qy 401 GlnArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProPheGlnPro 420  
 Db 1528 GCGCGCTTTCCTCCAGAGCTTACAGCGCCCACTGCTGCGAGCCAGCCATGAGCT 1587  
 Qy 421 GlnAsnLeuAspLeuGlnSerProThrLysLeuSerLysAlaSerGlnValAspSerThrIle 440  
 Db 1588 GAGAACTTGAACCTCCAGCTCCCAACCAAGCTGATGCCAGCGGAGGAGCTCCACATC 1647  
 Qy 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlnSerProArgSer 460  
 Db 1648 CCACAGCCAGCGCGCTCATATACATGCTTAAAGCTTCAAGAGGCTCTCCCGGAGC 1707  
 Qy 461 SerSerGlnSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlnSer 480  
 Db 1708 AGCAGCGAGAGCACTCAACCACTTACATGACACCCCGAAGTGCAGTCTCGGCTCT 1767  
 Qy 481 GlnSerProGlnHisAlaGlnMetCysLeuHisThrAlaGlnProThrPheAlaGlnGln 500  
 Db 1768 CAGTCCCGCAGCATGAGATGTGCTCCACACCGCTGCGCCAGGTTCTGCTGAGAG 1827  
 Qy 501 MetGlnGlnThrGlnSerGlnTyrSerAspSerSerCysGlnGlnGlnValAlaPhePheCys 520  
 Db 1828 ATGGAGAGAGCCAGCTGATGATCTCAATTTCTAGCTGTGAGAAAGGAGGCTTCTTGC 1887  
 Qy 521 AsnGlnCysAspCysArgPheSerGlnGlnAlaSerLeuLysArgHisThrLeuGlnThr 540  
 Db 1888 AATAGAGTGAATCGCGCTTCTGAGAGAGGCTCACTCAAGAGGAGCAAGCTGACAGC 1947  
 Qy 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlnAsn 560  
 Db 1948 CACAGTCAAAACCTTCAAGTGTGACCGCTGCGAGCGCTCTCCCTCAAGAGGAGAC 2007  
 Qy 561 LeuAlaSerHisLysThrValHisThrGlnGlnLysProTyrArgCysAsnIleCysGln 580  
 Db 2008 CTGCGCAGCCCAAGAGCGCTCATACCGGTGAGAAACCTTATCTGTGACATTTGTGGG 2067  
 Qy 581 AlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgLysHisSerGlnGlnLys 600  
 Db 2068 GCCAGATTCAACCGGCGAGCGCACTGAAACCAACCACTGAAATTCACTGTGAGAGAG 2127

Qy 601 ProTyrLysCysGlnThrCysGlnValAlaArgPheValGlnValAlaHisLeuArgHis 620  
 Db 2128 CCTTCAAAATGGGAACCTCGCGAGCCAGATTTGTACAGGTGGGCCACCTCGTCCAT 2187  
 Qy 621 ValLeuIleHisThrGlnGlnLysProTyrProCysGlnIleCysGlnThrArgPheArg 640  
 Db 2188 GTGCTTATCCACATCGTGTGAGAAAGCTTATCTCTGTGAATCTGTGGACCCGTTCGG 2247  
 Qy 641 HisLeuGlnThrLeuLysSerHisLeuArgHisHisThrGlnGlnLysProThrHisCys 660  
 Db 2248 CACCTTCAGACTCTAAGAGCCACTGGGAATCCACAGAGAAACCTTACCATTTGT 2307  
 Qy 661 GlnLysCysAsnLeuHisPheArgHisLysSerGlnLeuArgLeuHisLeuArgGlnLys 680  
 Db 2308 GAGAAATGATACCTGATTTCCGTCAAAAGCCAGCTGCGACTTCACTTGGCCAGAA 2367  
 Qy 681 HisGlnValIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700  
 Db 2368 CATGGGCGCATCAACCAAGGTGCAATCCGCTGTGAGCCAGCTGACCTGCTCCG 2427  
 Qy 701 GlnLeuProLysAlaCys 706  
 Db 2428 GAGCTCCCAAGCTGC 2445  
 RESULT 5  
 US-10-252-157-169/c  
 ; Sequence 169, Application US/10252157  
 ; Publication No. US20030190640A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Farris, Mary  
 ; TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER  
 ; FILE REFERENCE: PA-0027-1 US  
 ; CURRENT APPLICATION NUMBER: US/10/252,157  
 ; PRIOR FILING DATE: 2002-10-01  
 ; PRIOR APPLICATION NUMBER: 60/295,048  
 ; PRIOR FILING DATE: 2001-05-31  
 ; NUMBER OF SEQ ID NOS: 501  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 169  
 ; LENGTH: 4506  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; NAME/KEY: misc\_feature  
 ; OTHER INFORMATION: Incyte ID No. US20030190640A1 977470.16c  
 US-10-252-157-169  
 Alignment Scores:  
 Pred. No.: 0 Length: 4506  
 Score: 3777.00 Matches: 703  
 Percent Similarity: 99.7% Conservative: 1  
 Best Local Similarity: 99.6% Mismatches: 2  
 Query Match: 99.6% Indels: 0  
 DB: 6 Gaps: 0  
 US-10-755-889-18 (1-706) x US-10-252-157-169 (1-4506)  
 Qy 1 MetAlaSerProAlaAspSerCysIleGlnPheThrArgHisAlaSerAspValLeuLeu 20  
 Db 3219 ATGGCTCGCGCGCTGACAGCTGATCCAGTTCAACCGCCATGCCAGTATGTTCTTCTC 3160  
 Qy 21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValValIleValAlaSerArg 40  
 Db 3159 AACCTTAATCGTCTCCGAGTGGAGACATCTTGACATGATGTGTCTGTGAGCCGT 3100  
 Qy 41 GlnGlnPheArgAlaHisLysThrValLeuMetAlaCysSerGlnLeuPheTyrSerIle 60  
 Db 3099 GAGCAGATTAGACCCCATTAACAGGTCTCATGGCTGCAAGTGGCTGTTCTTATACATC 3040  
 Qy 61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGlnIleAsnPro 80

Db 3039 TTTACAGACCACTTGAATGCACTTAGTGATCATCTAGATCCTGAGATCAACCT 2980  
 Qy 81 GluGlyPheCysIleLeuLeuAspPheMetTyThrSerArgLeuAsnLeuArgGly 100  
 Db 2979 GAGGATTTCTGCATCTCTCTGATCATCTGCTCACTCTGCTCAATTTGGGAGAGGC 2920  
 Qy 101 AsnIleMetAlaValMetAlaThrAlaMetTyThrLeuGlnMetGlnIleValAlaPThr 120  
 Db 2919 AACATCATGTGCTGTGATGGCCACCGCTATATCTGAGATGAGGAGCATGTTGTGAGCACT 2860  
 Qy 121 CysArgIysPheIleValAlaSerGluAlaGluMetValSerAlaIleValProProArg 140  
 Db 2859 TGGCGAAGATTATTATAGCCAGATGAGAGAGATGTTTCTGCACTACAGCTCTCTGT 2800  
 Qy 141 GluGluPheLeuAsnSerArgMetLeuMetProGlnAspIleMetAlaTyArgGlyArg 160  
 Db 2799 GAAGAGTTCTTCACAGCCGAGATCTGATGCCCAAGACATCATGCTCATCGGGTCTGT 2740  
 Qy 161 GluValValGluAsnAsnLeuProLeuArgSerAlaProGlyCysGlnSerArgAlaPhe 180  
 Db 2739 GAGGTGTGTGAGAACCACTTCCACTGAGAGCGCCCTGGGTGTGAGAGAGAGAGCTTT 2680  
 Qy 181 AlaProSerLeuTySerGlyLeuSerThrProProAlaSerTySerMetTySerHis 200  
 Db 2679 GCGCCAGACCTGTACAGTGGCTCTGTCCACCGCCAGCTCTTATTCATCTACAGCCAC 2620  
 Qy 201 LeuProValSerSerLeuLeuPheSerAspGluGluPheArgAspValArgMetProVal 220  
 Db 2619 CTCCTGTACAGACAGCTCTCTCTTCCGATGAGAGATTCCGAGATGTCGGATGCTGTG 2560  
 Qy 221 AlaAsnProPheProLeuArgGluArgAlaLeuProCysAspSerAlaArgProValProGly 240  
 Db 2559 GCCAACCCCTTCCCAAGAGACCGGGCACTCCCATGTGATGTAGTCCAGGCCAGTCCCTGT 2500  
 Qy 241 GluTySerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTySer 260  
 Db 2499 GAGTACAGCCGCGCACTTGTGAGGTGTCCCAATGTGTGCACAGCAAAATCTATTCA 2440  
 Qy 261 ProIysGluThrIleProGluGluAlaArgSerAspMetHisTySerValAlaGluGly 280  
 Db 2439 CCGAAGAAACATCTCCAGAAAGAGCAGAACTGATATGCACTACAGTGTGGCTGAGGCG 2380  
 Qy 281 LeuIysProAlaAlaProSerAlaArgAsnAlaProTyPheProCysAspIysAlaSer 300  
 Db 2379 CTCAACCTGTGCTGCTCTCTGAGCCGGAATGCCCCCTACTTCCCTGTGACAGAGCCAGC 2320  
 Qy 301 LysGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAsn 320  
 Db 2319 AAAGAAAGAGAGACCTCTCTCGGAAGATGATGTGCTGCAATTTGAGGCCCCCAT 2260  
 Qy 321 AlaProLeuAsnArgIysGlyLeuValSerProGlnSerProGlnIysSerAspCysGln 340  
 Db 2259 GCACCCCTGAAACCGAAGGGTGTGTATGTCACAGAGCCCCCAGAAATCTGACTGCCAG 2200  
 Qy 341 ProAsnSerProThrGluAlaCysSerSerIysAsnAlaCysIleLeuGlnAlaSerGly 360  
 Db 2199 CCGAAGTGGCCCAAGAGTCTGAGCAGAGTAAAGATGCTGATCTCCAGGCTTCTGAGC 2140  
 Qy 361 SerProProAlaIysSerProThrAspProIysAlaCysAsnTyrIleValTyPhe 380  
 Db 2139 TCCCTCCAGCCCAAGAGCCCACTAACCCCAAGCTGCACTGAAAGAAATCAAGTTC 2080  
 Qy 381 IleValLeuAsnSerLeuAsnGlnAsnAlaIysProGlyGlyProGluGlnAlaGluLeu 400  
 Db 2079 ATCTGTCTCAACAGCTCTCAATCAATGCAAAACAGAGGGGCTGAGAGAGCTAGAGCTG 2020  
 Qy 401 GlyArgLeuSerProArgAlaTyThrAlaProProAlaCysGlnProProMetGluPro 420  
 Db 2019 GGCCTGCTTCCCAAGAGCTTACAGGCCCCCAGCTGCTGCAAGCCCATGAGAGCTT 1960  
 Qy 421 GluAsnLeuAspLeuGlnSerProThrIysLeuSerAlaSerGlyGluAspSerThrIle 440  
 Db 1959 GAGAACTTTGACTCCAGTCCCAACCAAGCTGAGTGCAGCGGAGAGAGATCCACCATC 1900

Qy 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460  
 Db 1899 CCAAGAGCCAGCCGGCTCAATTAACATCTTTACAGATTCATGACGGGCTTCCCGCAGC 1840  
 Qy 461 SerSerGluSerHisSerProLeuTyThrMetHisProProIysCysThrSerCysGlySer 480  
 Db 1839 AGCAGGAGAGAGCCACTACACATCTTACATGACCCCCGGAAGTGCAGTCTCGGCTCT 1780  
 Qy 481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGln 500  
 Db 1779 CAGTCCCAAGCAGATGAGATGTGCTTCCACACCGCTGCGCCACAGTTCCTTGAGAG 1720  
 Qy 501 MetGlyGluThrGlnSerGluTyThrAspSerSerCysGlnAsnGlyAlaPhePheCys 520  
 Db 1719 ATGGAGAGAGCCAGTGTGATCTAGATTTCACTGATCTGATGAGAAAGGGGCTTCTTTC 1660  
 Qy 521 AsnGlyCysAspCysArgPheSerGluGluAlaSerLeuIysAlaArgHisThrLeuGlnThr 540  
 Db 1659 AATGAGTGTACGTGCGCTTCTCTGAGAGAGCTCACTCAAGAGGCACAGCTGCAAGAC 1600  
 Qy 541 HisSerAspIysProTyThrCysAspArgCysGlnAlaSerPheArgTyThrGlyAsn 560  
 Db 1599 CACAGTACAAACCTTACAAAGTGTGACCGCTGCGAGGCTCTTCCGCTCAAGAGGCAAC 1540  
 Qy 561 LeuAlaSerHisIleTyThrValHisThrGlyGluIysProTyArgCysAsnIleCysGly 580  
 Db 1539 CTCGCGACCAACAGACCGTTCATCCGTGAGAAACCTTATGCTTCCATCTGAGAGAG 1480  
 Qy 581 AlaGlnPheAsnArgProAlaAsnLeuIysThrHisThrArgIleHisSerGlyGluIys 600  
 Db 1479 GCCAGTTCAACCGCGCAGCAACCTGAAAACCACTGAAATTCATCTGAGAGAGAG 1420  
 Qy 601 ProTyThrCysGluThrTyCysGlyAlaArgPheValGlnValAlaHisIleValAlaHis 620  
 Db 1419 CCTACAAATGCGAAACCTGCGAGGAGCAATTTGTACAGGTGGCCCACTCCGCGCCAT 1360  
 Qy 621 ValLeuIleHisThrGlyGluIysProTyProCysGluIleCysGlyThrArgPheArg 640  
 Db 1359 GTGCTTATCCACATGTGTGAGAGCCCTTATCCGTGAATGTGTGACCCGTTCCGG 1300  
 Qy 641 HisLeuGlnThrLeuIysSerHisIleLeuArgIleHisThrGlyGluIysProTyHisCys 660  
 Db 1299 CACCTTACAGCTTGAAGAGCCACTGCGAATCCACACAGAGAAACCTTACATTTGT 1240  
 Qy 661 GluIysCysAsnLeuHisPheArgHisIysSerGlnLeuArgLeuHisIleValArgGlnIys 680  
 Db 1239 GAGAAGTGTACCTGATTTCCGTCAAAAAGCCAGCTGGCACTTCACTTCCGCGCAGAG 1180  
 Qy 681 HisGlyAlaIleThrAsnThrIysValGlnTyArgValSerAlaThrAspLeuProPro 700  
 Db 1179 CATGGCGCATCACCAACCAACAGGTGCATATCCGCGTGCAGCTGACTGACTGCTCCG 1120  
 Qy 701 GluLeuProIysAlaCys 706  
 Db 1119 GAGCTCCCAAGGCTGC 1102

# RESULT 6

US-09-107-058-1  
 Sequence 1, Application US/09107058  
 Patent No. US20010010922A1  
 GENERAL INFORMATION:  
 APPLICANT: Dalla-Favera, Riccardo  
 APPLICANT: Niu, Hui-Feng  
 TITLE OF INVENTION: CLONING AND USES OF THE GENETIC  
 TITLE OF INVENTION: LOCUS bcl-6  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America

```

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,058
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: 422523 COOP U
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3720 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 328..2445
US-09-107-058-1

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Db 1888 AATGAGTGTGACTCCGCTTCTCTGAGAGGCTCACTCAAGAGCAACGCTGCAACC 1947  
 Qy 541 HisSerAspIysProTyrIleYsAspArgCysGlnAlaSerPheArgTyrIleGlyAsn 560  
 Db 1948 CAGAGTCAAAACCTTCAAGTGTGACCGCTGCGAGGCTCTCCCTCAAGAGGCAAC 2007  
 Qy 561 LeuAlaSerHisIleThrValHisThrGlyGlnIleYsProTyrArgCysAsnIleCysGly 580  
 Db 2008 CTCGCCAGCCCAAGACCGCTTCAACCGGTGAGAAACCTATCTGTCAACATCTGTGG 2067  
 Qy 581 AlagIlnPheAsnArgProAlaAsnIleuIleThrHisThrArgIleHisSerGlyIleuYs 600  
 Db 2068 GCCCAGTTCAACCGGCCAGCCCACTGAAACCACTGAACTTCACTCTGGAGAGAG 2127  
 Qy 601 ProTyrIleYsCysGlnThrCysGlyAlaArgPheValGlnValAlaHisIleuArgAlaHis 620  
 Db 2128 CCCCACAAATGCCAAACCTGGGAGGACGAGATTGTATACGGGTGGCCACCTCGGCCCAT 2187  
 Qy 621 ValIleuIleHisThrGlyIleuYsProTyrProCysGlnIleCysGlyThrArgPheArg 640  
 Db 2188 GTGCTTATCCACACTGGGTGAGAAAGCCCTATCCCTGTGAAATCTGTGGCAACCCGTTCCGG 2247  
 Qy 641 HisIleuIlnThrIleuYsSerHisIleuArgIleHisThrGlyIleuYsProTyrHisCys 660  
 Db 2248 CACCTTCAAGCTTGAAGAGCCACCTGGAATCCACAGAGAGAAACCTTACCATTTGT 2307  
 Qy 661 GluIleYsAsnIleuHisPheArgHisIleYsSerGlnIleuArgIleuHisIleuArgGlnIleYs 680  
 Db 2308 GAGAGGTGTAACCTGCACTTCCGTCACAAAGCCAGCTGCGACCTTCACTTGGCGCAAGAG 2367  
 Qy 681 HisGlyAlaIleThrAsnThrIleYsValGlnTyrArgValSerAlaThrAspIleuProPro 700  
 Db 2368 CATGGCGCATCAACCAACCAAGGTGCAATACCGCTGACGACCTGACCTGCTCCG 2427  
 Qy 701 GluIleuProIleYsAlaCys 706  
 Db 2428 GAGCTCCCAAGCCTGC 2445

## RESULT 7

US-09-761-117-1  
 Sequence 1, Application US/09761117  
 Patent No. US20010012887A1

## GENERAL INFORMATION:

APPLICANT: Dalia-Favera, Riccardo  
 Chaganti, Raju S.K.

TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS  
 bcl-6

NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York

STATE: New York  
 COUNTRY: United States of America

ZIP: 10036

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/761,117  
 FILING DATE: 16-Jan-2001

CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:

NAME: White, John P.  
 REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400  
 TELEFAX: (212) 391-0525

TELEFAX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 3720 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 328..2445  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-761-117-1

Alignment Scores:

Pred. No.: 0 Length: 3720  
 Score: 3763.00 Matches: 701  
 Percent Similarity: 99.4% Conservative: 1  
 Best Local Similarity: 99.3% Mismatches: 4  
 Query Match: 99.2% Indels: 0  
 DB: 3 Gaps: 0

US-10-755-889-18 (1-706) x US-09-761-117-1 (1-3720)

Qy 1 MetAlaSerProAlaAspSerCysIleGlnPheThrArgHisAlaSerAspValIleuLeu 20  
 Db 328 ATGGCTCGCGCGCTGACAGCTGTATCCAGTTCACCGGCATGCGAGGATGTTCTTCTC 387  
 Qy 21 AsnIleuAsnArgIleuArgSerArgAspIleIleuThrAspValIleValIleValSerArg 40  
 Db 388 AACCTTATGCTCTCCGAGTCCAGACATCTTGACTGATGTTGTGAGAGCGGT 447  
 Qy 41 GluGlnPheArgAlaHisIleYsThrValIleuMetAlaCysSerGlyIleuPheYrSerIle 60  
 Db 448 GAGAGATTGAGACCCCAATAAAGCTCTATGAGCTCGAGAGAGCGCTGTTCTATGACATC 507  
 Qy 61 PheThrAspGlnIleuYsCysAsnIleuSerValIleAsnIleuAspProGlnIleAsnPro 80  
 Db 508 TTTRACAGACAGTTGAAATGCAACCTTAGTGATGATCAATGATCTGATGATCAACCT 567  
 Qy 81 GluGlyPheCysIleIleuIleuAspPheMetIleThrSerArgIleuAsnIleuArgGlnGly 100  
 Db 568 GAGGATTTGATCCTCTGACCTTCATGATACATCTGCGCTCAATTTGCGGAGAGGC 627  
 Qy 101 AsnIleuMetAlaValMetAlaThrIleuGlnIleuGlnIleuGlnIleuGlnIleuGlnIleu 120  
 Db 628 AACCTTATGCTCTCCGAGTCCAGACATCTTGACTGATGTTGTGAGAGCGGT 687  
 Qy 121 CysArgIleuPheIleYsAlaSerGlnAlaGlnMetValSerAlaIleYsProProArg 140  
 Db 688 TGCCGAAATTATTAAGGCCAGTGAAGAGAGATGTTCTGCAATCAAGCTCTCTGT 747  
 Qy 141 GluGlnPheIleuAsnSerArgMetIleuMetProGlnAspIleuMetAlaIleYsArgGlyArg 160  
 Db 748 GAAGATTCTTCAACAGCCGAGATGCTGATGCCCAAGACATCATGCGGCTCGT 807  
 Qy 161 GluValValGlnIleuAsnIleuProIleuArgSerAlaProGlyCysGlnIleuArgAlaPhe 180  
 Db 808 GAGGTGTGAGAAACAACCTGCACTGAGAGAGCCCTCGGTGTGAGAGAGAGCTT 867  
 Qy 181 AlaProSerIleuYrSerGlyIleuSerThrProProAlaSerIleYsSerMetIleYsSerHis 200  
 Db 868 GCCCCAGCCGTGACAGTGGCTGTCCACACCGCCAGCTCTTATTCATGTACAGCCAC 927  
 Qy 201 LeuProValSerSerIleuIleuPheSerAspGlnIleuArgAspValIleuArgMetProVal 220  
 Db 928 CTCCTGTGAGCAACCTCTCTTCTCGAGAGAGAGTTGGAGATGTCGGATCGCTGTG 987  
 Qy 221 AlaAsnProPheProIleuArgAlaIleuProCysAspSerAlaArgProValProGly 240  
 Db 988 GCCAACCCCTTCCCAAGAGAGCGGCACTCCCATGTATGTGACAGCCAGTCCCTGTG 1047  
 Qy 241 GluIleYsSerArgProIleuGlnValIleuSerProAsnValCysHisSerAsnIleYrSer 260  
 Db 1048 GAGTACAGCCGCGGACTTGTGAGAGTGTCCCAATGTGTGCCACAGCAATATCTATTCA 1107

QY 261 ProlyseGluThrIleProGluGluAlaArgSerAspMetHisTyrSerValAlaGluGly 280  
DB 1108 CCCAAGAAACATCCCAAGAGGACAGAGTGAATGCACTACAGTGGCTGGAGGGC 1167  
QY 281 LeuLeuProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLeuAlaSer 300  
DB 1168 CTCGAACCTGCTGCTCCCTCAGCCCGAATGGCCCTCTACTCTCTGTGACAGGCGCAG 1227  
QY 301 LysGluGluGluArgProSerSerGluArgGluIleAlaLeuHisPheGluProProAsn 320  
DB 1228 AAAAGAGAGAGAGAGCCCTCTCGAGAGATGGATTCCTTCGATTCGAGCCCTCAT 1287  
QY 321 AlaProLeuAsnArgLysGluLeuValSerProGlnSerProGlnLysSerAspCysGln 340  
DB 1288 GCAACCTCTGAACGAGAGGGGTGTGTTAGTCCAGAGCCCTCGAAGATTCGCTGCCAG 1347  
QY 341 ProAsnSerProThrGluAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSerGly 360  
DB 1348 CCCAAGCTGGCCCAAGAGGCTGAGAGCATGATGCTTCCTCCAGGGTCTGGC 1407  
QY 361 SerProProAlaLysSerProThrAspProLysAlaCysAsnTrpLysTyrLysPhe 380  
DB 1408 TCCCTCTCAGCCCAAGAGCCCTCAGACCCCAAGCCCTGAGGAGAAATCAAGTTC 1467  
QY 381 IleValLeuAsnSerLeuAsnGlnAsnAlaLysProGlyGluProGlnAlaGluLeu 400  
DB 1468 ATCTGCTTCACAGCCTTCACAGATGCAAGATCCAAACAGAGGGGCTGAGAGGCTGAG 1527  
QY 401 GlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProPheGluPro 420  
DB 1528 GGGCGCTTTCCTCCAGAGGCTACAGCGCCCACTGCTGCGCAGCCACCATGAGGCT 1587  
QY 421 GluAsnLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIle 440  
DB 1588 GAGAACTTCAGCCTCCAGTCCCAACCAAGCTGATGCCAGCGGAGGAGCTCACCATC 1647  
QY 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460  
DB 1648 CCACAAACCGAGCGCTCAATACATGATGATGATGATGATGATGATGATGATGATGAT 1707  
QY 461 SerSerGluSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480  
DB 1708 AGCAGGAGAGGAGCCTACCACTCTATAGTACACCCCGAAGTGCATGCTCGGCTCT 1767  
QY 481 GlnSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGluGlu 500  
DB 1768 CAGTCCCAACAGCATGAGAGATGCTCCACACCCCTGCGCCACAGTTCGCTGAGAG 1827  
QY 501 MetGlyGluThrGlnSerGluTyrSerAspSerSerCysGluAsnGlyAlaPhePheCys 520  
DB 1828 ATGGAGAGAGCCAGCTGAGTACTGAGATTCAGATTCAGTGTGAGAAAGGAGGCTCTT 1887  
QY 521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuLysArgHisThrLeuGlnThr 540  
DB 1888 AATAAGTGTGCTGCTGCTCTCTGAGAGGCTCATCTCAAGAGGACAGCTGACAC 1947  
QY 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGlyAsn 560  
DB 1948 CACAGTACAAACCTCAAGTGTGACCGCTGCGCAGGCTCTCCCTCAAGAGGAC 2007  
QY 561 LeuAlaSerHisLysThrValHisThrGlyGluLysProTyrArgCysAsnIleCysGly 580  
DB 2008 CTGCGCAGCCACAGACCGTTCATACCGGTGAGAAACCTTCCTGACATCTGTGGG 2067  
QY 581 AlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgIleHisSerGlyGluLys 600  
DB 2068 GCCAAGTTCACCGGCGCAGCCACCTGAAAACCAACTGGAATTCATCTCGAGAGAG 2127  
QY 601 ProTyrLysCysGluThrCysGlyAlaArgPheValGlnValAlaHisLysLeuArgAlaHis 620  
DB 2128 CCTCAAAATGTCGAAACCTGCGGAGCAGATTTGTACAGGTGGCCCACTCCGCTCAT 2187

QY 621 ValLeuIleHisThrGlyGluLysAspProTyrProCysGluIleCysGlyThrArgPheArg 640  
DB 2188 GTGCTTATCCACACTGAGAGAGCCCTATCCCTGTGAATCTGTGGACCCGTTCCGG 2247  
QY 641 HisLeuGlnThrLeuLysSerHisLysLeuArgIleHisThrGlyGluLysProTyrHisCys 660  
DB 2248 CACTTCAGACTCTGAAGGACCACTGCGAATCCACAGGAGAGAAACCTTACATGAT 2307  
QY 661 GluLysCysAsnLeuHisPheArgHisLysSerGlnLeuArgLeuHisLysArgGlnLys 680  
DB 2308 GAGAGGTGATCTGATTCATTCCTGTCACAAAGCCAGCTGCACTTCCTGCGCAGAG 2367  
QY 681 HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700  
DB 2368 CATGGGCGCATCACCAACCAAGGTGCAATACCGGTGTGAGCCACTGACCTGCCG 2427  
QY 701 GluLeuProLysAlaCys 706  
DB 2428 GAGCTCCCAAGGCTGC 2445

RESULT 8  
US-10-295-027-15  
Sequence 15, Application US/10295027  
Publication No. US2003023250A1  
GENERAL INFORMATION:  
APPLICANT: Afar, Daniel  
APPLICANT: Aziz, Natasha  
APPLICANT: Gish, Kurt C.  
APPLICANT: Gish, Kurt C.  
APPLICANT: Glynne, Richard  
APPLICANT: Hevezl, Peter A.  
APPLICANT: Mack, David H.  
APPLICANT: Murray, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Ros Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer  
FILE REFERENCE: 018501-012500US  
CURRENT APPLICATION NUMBER: US/10/295,027  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: US 09/663,733  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 60/350,666  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/335,394  
PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: US 60/332,464  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: US 60/334,393  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: US 60/340,376  
PRIOR FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: US 60/347,211  
PRIOR FILING DATE: 2002-01-08  
PRIOR APPLICATION NUMBER: US 60/347,349  
PRIOR FILING DATE: 2002-01-10  
PRIOR APPLICATION NUMBER: US 60/355,250  
PRIOR FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: US 60/356,714  
PRIOR FILING DATE: 2002-02-13  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1386  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 3676  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-295-027-15

Alignment Scores:  
Pred. No.: 2,55e-97 Length: 3676  
Score: 1155.00 Matches: 268  
Percent Similarity: 46.6% Conservative: 58

Best Local Similarity: 38.3% Mismatches: 142  
 Query Match: 30.5% Indels: 232  
 DB: 6 Gaps: 15

US-10-755-889-18 (1-706) x US-10-295-027-15 (1-3676)

QY 1 MetLaserProAla-----AspSerCysIle-----GlnPheThrArgHis 14  
 DB 141 ATGGGTTTCCCGCGCGCCGAGAGAGGCTGAGCTACGTCGCGAGTTTACTCGGCAC 200  
 QY 15 AlaSerAPValIleuLeuAsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspVal 34  
 DB 201 TCCTCCAGCTGCTGGGCACTCAACAGAGCTGGCGCTGGCGGAGATCTCATCGAGCTC 260  
 QY 35 ValIleValIleSerArgGlnGlnPheArgAlaHisIleYThrValIleuMetAlaCysSer 54  
 DB 261 ACGTGTGCTGGTGGCGGCAACCCCTCAGAGACACAGAGAGGATTCATCGCTGAGCT 320  
 QY 55 GlyLeuPheTySerIlePheThrAspGlnLeuIleCysAsnLeuSerValIleAsnLeu 74  
 DB 321 GGCTTCTTCTATTCATTTTCCGGGCGCTGCGGAGTCCGGGCTGGAAGTCTCTCTG 380  
 QY 75 AspProGluIleAsnProGluGlnIlePheCysIleLeuLeuAspPheMetTyThrSerArg 94  
 DB 381 CCCGGGGGTCCCGAAGCAGAGGCTTCGCCCTCTATTGGACTTATGATCACTTCGCGC 440  
 QY 95 LeuAsnLeuArgGlnIleAsnIleMetAlaValMetAlaThrAlaMetTyLeuGlnMet 114  
 DB 441 CTGGGCGCTCTCCAGCAGCAGCAGCAGCAGCAGCTTCAGGCGCGCCACCTATTGCAAGTG 500  
 QY 115 GlnHisValIleValAspThrCysArgIlePheIleIleValAspGlnIleValSer 134  
 DB 501 GAGCAGCTGGTCCAGGCACTGCCACCGCTTCATCCAGGCGCAGC----- 542  
 QY 135 AlaIleIleYProProArgGlnGlnIlePheLeuAsnSerArgMetLeuMetProGlnAspIle 154  
 DB 542 ----- 542  
 QY 155 MetAlaTyArgGlyArgGluValValGlnAsnAsnLeuProLeuArgSerAlaProGly 174  
 DB 542 ----- 542  
 QY 175 CysGlnSerArgAlaPheAlaProSerLeuTySerGlyLeuSerThrProProAlaSer 194  
 DB 542 ----- 542  
 QY 542 ----- 542  
 QY 195 TySerMetTySerHisLeuProValSerSerLeuLeuPheSerAspGlnIlePheArg 214  
 DB 543 -----TATGAACCTCTGGGCATCTCC----- 563  
 QY 215 AspValArgMetProValAlaAsnProPheProIleGlyArgAlaLeuProCysAspSer 234  
 DB 563 ----- 563  
 QY 235 AlaArgProValProGlyGlnTySerArgProThrIleGlnValSerProAsnValCys 254  
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 QY 255 HisSerAsnIleTySerProIleGlnThrIleProGlnGlnAlaArgSerAspMetHis 274  
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 QY 275 TyrSerValAlaGlnGlyLeuAspProAlaAlaProSerAlaArgAsnAlaProTyRhe 294  
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 QY 295 ProCysAspIleAlaSerIleGlnGlnIleGlnIleProSerSerGlnAspGlnIleAlaLeu 314  
 DB 576 -----GAGCAGAGAACCCCAACA----- 593  
 QY 315 HisPheGlnProProAsnAlaProLeuAsnArgIleGlyLeuValSerProGlnSerPro 334  
 DB 594 -----CCCCCAAGGCGCT-----CCACCAAGTATGATCC 623

QY 335 GlnTySerAspCysGlnProAsnSerProThrGlnAlaCysSerSerIleAsnAlaCys 354  
 DB 624 AGGCGCTCCGAGAGACACCCAGACCCACTTACGATTCGAGAC----- 668  
 QY 355 IleLeuGlnAlaSerGlySerProProAlaIleYSerProThrAspProIleValCysAsn 374  
 DB 669 -----TGCAATCAAGGCCCCCAGAGCCAGCCAGCCCTGACCCCAAGGCGCTGAC 719  
 QY 375 TrpIleYsTyIlePheIleValIleAsnSerLeuAsnGlnIleAsnAlaIleProGlyGly 394  
 DB 720 TGGAAAAAGTAAAGTAAATCGGTAAACTCT----- 752  
 QY 395 ProGlnGlnAlaGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 414  
 DB 753 -----CAGGCTCCCAAGAGAGAGCTGTGGGAGAGAAAGTTCTGCTCACTTGGCCCC 809  
 QY 415 GlnProMetGlnProGlnIleAsnLeuAspLeuGlnIleSerProThrIleValSerAlaSer 434  
 DB 810 CAAAGCAGGCTCCCAAGTGAAGAGAGGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 869  
 QY 435 GlyIleAspSerThrIlePro---GlnAlaSerArgLeuAsnIleValAsnArgSer 453  
 DB 870 AGTGAAG 908  
 QY 454 MetThrGlySerProArgSerSerSerGlnSerHisSerProLeuTyMetHisProPro 473  
 DB 909 -----TCTCAACTGCTCCAGCTGTCAGTTC----- 935  
 QY 474 LysCysThrSerCysGlySerGlnSerProGlnHisAlaGlnMetCysLeuHisThrAla 493  
 DB 936 -----AAATGTGG-----GCTCCAGCAGAGTACCCCTCATCTCATCTCCAG 980  
 QY 494 GlyProThrPheAlaGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 513  
 DB 981 -----GCTCAAGACACTGTGATCACTCTGAACCGCTCTGCTCACTACCG 1028  
 QY 514 GlnAsnGlyAlaPhePheCysAsnGlnCysAspCysArgPheSerGlnIleValSerIleu 533  
 DB 1029 GGAAGTGAATTTTCACTGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1088  
 QY 534 LysArgHisThrIleGlnIleThrHisSerAspIleProIleCysArgAspCysGlnAla 553  
 DB 1089 GAC---TCTTGGTCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 1145  
 QY 554 SerPheArgTyIleGlyAsnLeuAlaSerHisIleTyThrValHisThrGlyGlnIlePro 573  
 DB 1146 TCGTTCCGCTACAGAGGCAACCTTGCCAGTCATCTGACAGTGCACAGAGGGAAGAGCT 1205  
 QY 574 TyArgCysAsnIleCysGlyAlaGlnPheAsnArgProAlaAsnIleTyThrHisThr 593  
 DB 1206 TACCACTGCTCAATCTCGGAGCGCGGCTTTAAACCGGAGAGAGAGAGAGAGAGAGAG 1265  
 QY 594 ArgIleHisSerGlyGlnIleProTyIleCysGlnIleThrCysGlyAlaArgPheValGln 613  
 DB 1266 CGCATCAATCGGAG 1325  
 QY 614 ValAlaHisLeuArgAlaHisValIleIleHisThrGlyGlnIleProTyProCysGln 633  
 DB 1326 GTGGCAATCTGGGGGAG 1385  
 QY 634 IleCysGlyThrArgPheArgHisLeuGlnIleThrIleIleValSerHisIleValIle 653  
 DB 1386 ACGTGGAG 1445  
 QY 654 GlyGlnIleProTyIleCysGlyIleCysAsnLeuHisPheArgHisIleSerGlnIleu 673  
 DB 1446 GGAAG 1505  
 QY 674 ArgLeuHisLeuArgGlnIleValIleThrAsnThrIleValGlnTyArgVal 693  
 DB 1506 CGGCTGATCTGGCGAG 1565



## RESULT 9

US-10-211-462-23  
Sequence 23, Application US/10211462  
Publication No. US2004003495A1  
GENERAL INFORMATION:  
APPLICANT: Murray, Richard  
APPLICANT: Glysne, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Atiz, Natcha  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and  
FILE REFERENCE: 018501-006200US  
CURRENT APPLICATION NUMBER: US/10/211,462  
CURRENT FILING DATE: 2003-02-13  
PRIOR APPLICATION NUMBER: US 09/784,356  
PRIOR FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: US 09/791,390  
PRIOR FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: US 60/310,025  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: US 60/334,244  
NUMBER OF SEQ ID NOS: 230  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 23  
LENGTH: 3676  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-211-462-23

## Alignment Scores:

Pred. No.: 2.55e-97 Length: 3676  
Score: 1155.00 Matches: 268  
Percent Similarity: 46.6% Conservative: 58  
Best Local Similarity: 38.3% Mismatches: 142  
Query Match: 30.5% Indels: 232  
DB: 7 Gaps: 15

US-10-755-889-18 (1-706) x US-10-211-462-23 (1-3676)

QY 1 MetAlaSerProAla-----AspSerCysIle-----GlnPheThrArgHis 14  
DB 141 ATGGGTTCCCGCCCGCCCGGAGGAGCGCTGGGCTACGTCGCGAGTTCACTCCGCGAC 200  
QY 15 AlaSerApValIleuLeuAenLeuAenArgLeuArgSerArgApIleuThrArgVal 34  
DB 201 TCCTCCGACGTGCTGGGCAACCTCAACGAGCTGGCGCGGAGATCTCACTGACGTC 260  
QY 35 ValIleValIleSerArgGluGlnPheArgAlaHisIleThrValIleuMetAlaCysSer 54  
DB 261 ACGGTGCTGGTGGCGGCAACCCCTCAGACACAAAGGCAAGTTCATCGCTGAGT 320  
QY 55 GlysLeuPheTyrSerIlePheThrAspGlnLeuLysCysAenLeuSerValIleAenLeu 74  
DB 321 GGCTTCTTCTATTCAATTTTCCGGGCGCTGCGGAGTCCGGGAGTGCAGCTCTCTG 380  
QY 75 AspProGluIleAenProGluGlyPheCysIleLeuLeuAenPheMetTyrThrSerArg 94  
DB 381 CCGGAGGAGTCCGAGGAGGAGGCTTCGCGCCCTGATTTGACTTCATGACATTGCGCG 440  
QY 95 LeuAenLeuArgGluGlyAenIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMet 114  
DB 441 CTGGCGCTCTCTCCAGCAGCTGACCCAGCTCTTACGCGCGCCACCTATTGCAAGATG 500  
QY 115 GluHisValIleAspThrCysArgLysPheIleLysAlaSerGluAlaGluMetValSer 134  
DB 501 GAGCAGCTGCTCCGAGCATGACCGCTTCACTCCAGGCGAC-----542  
QY 135 AlaIleLysProArgArgGluGluPheLeuAenSerArgMetLeuMetProGlnAspIle 154  
DB 542 -----542

QY 155 MetAlaTyrArgGlyArgGluValValGluAenAenLeuProLeuArgSerAlaProGly 174  
DB 542 -----542  
QY 175 CysGluSerArgAlaPheAlaProSerLeuTyrSerGlyLeuSerThrProProAlaSer 194  
DB 542 -----542  
QY 195 TyrSerMetTyrSerHisLeuProValaSerSerLeuAenPheSerAspGluGluPheArg 214  
DB 543 -----TATGAACCTCTGGGCACTTC-----563  
QY 215 AspValArgMetProValaAlaAenProPheProLysGluArgAlaLeuProCysAspSer 234  
DB 563 -----563  
QY 235 AlaArgProValaProGluGlyTyrSerArgProThrLeuGluValSerProAenValCys 254  
DB 563 -----563  
QY 255 HisSerAenIleTyrSerProLysGluThrIleProGluGluAlaArgSerAspMetHis 274  
DB 563 -----563  
QY 275 TyrSerValAlaGluGlyLeuLysProAlaAlaProSerAlaArgAenAlaProTyrPhe 294  
DB 564 -----CTGGCGCCCTCG-----575  
QY 295 ProCysAspLysAlaSerLysGluGluArgProSerSerGluAspGluIleAlaLeu 314  
DB 576 -----GAAGCAGAACCCCAACA-----593  
QY 315 HisPheGluProProAenAlaProLeuAenArgLysGlyLeuValSerProGlnSerPro 334  
DB 594 -----CCCCCAACGGCCCT-----CCACCAAGTACTGCC 623  
QY 335 GlnLysSerAspCysGlnProAenSerProThrGluAlaCysSerSerLysAenAlaCys 354  
DB 624 AGCGCTCCGAAGACACCCAGACCCACTACTGATCTGAAAGC-----668  
QY 355 IleLeuGlnAlaSerGlySerProProAlaLysSerProThrAspProLysAlaCysAen 374  
DB 669 -----TGCAATCAAGCCCGCCAGCTCCAGCAGCCGTCAGCCCAAGGCTTGCAC 719  
QY 375 ThrLysLysTyrLysPheIleValLeuAenSerLeuAenGlnAenAlaLysProGlyGly 394  
DB 720 TGGAAAAAGTACAGTACATCGTCTAAACTCT-----752  
QY 395 ProGluGlnAlaGluLeuGlyArgLeuSerProArgAlaTyrThrAlaProProAlaCys 414  
DB 753 ---CAGGCTCCCAACAGGAGACCTGTCGGGAGAGAAAGTTCTGCTCACTTCCGCC 809  
QY 415 GlnProMetGluProGluAenLeuAenPheLeuGlnSerProThrLysLeuSerAlaSer 434  
DB 810 CAAGCAGAGCTCCCAAGAGAGAGGCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 869  
QY 435 GlyLysAspSerThrIlePro---GlnAlaSerArgLeuAenIleValAenArgSer 453  
DB 870 AGTGAAGAAGAACCCCTTCTGCTCCCAAGAGAGCTC-----908  
QY 454 MetThrGlySerProArgSerSerGluSerHisSerProLeuTyrMetHisProPro 473  
DB 909 -----TCTCAACTGCTGCACTTGCAGTTC-----935  
QY 474 LysCysThrSerCysGlySerGlnSerProGlnIleAlaGluMetCysLeuHisThrAla 493  
DB 936 -----AAAGTGGG-----GCTCCAGCAGTAAACCCCTAATCTCATCATCCAG 980  
QY 494 GlyProThrPheAlaGluGluMetGlyGluThrGlnSerGluTyrSerAspSerCys 513  
DB 981 -----GCTAAGACACTTGGATTCACCTTGAAAGGAGGCTGTCCATCACG 1028  
QY 514 GluAenGlyAlaPhePheCysAenGluCysAspCysArgPheSerGluAlaSerLeu 533



Db 1029 GGAAGTAATTTTACCTCCAGAACTGTAGGCTGTGCGAGGCTCTCATTCGGGGCTG 1088  
Qy 534 LyeArghIsthrLeuGlnThrHisSerAspLysProTyrLysCysAspArgCysGlnAla 553  
Db 1089 GAC---TCCTTGCTGCTCGGGAGGAGAAACAAACCTTAAAGTGTCAAGCTGTGCGGCTCT 1145  
Qy 554 SerPheArghTyrLysGlnLeuAlaSerHisLysThrValHisThrGlnGluPro 573  
Db 1146 TCGTTCGGCTACAAAGGCAACCTTGCAGTCATGTCAAGTGCACACAGGGGAAAGCCT 1205  
Qy 574 TyrArgCysAsnLysCysGlnAlaGlnPheAsnArgProAlaAsnLysThrHisThr 593  
Db 1206 TACACAGCTCAACTCCGAGCCCGGTTTAAACCGGACGAAACCTGAAACCGACAGC 1265  
Qy 594 ArgLHisSerGlnGlnLysProTyrLysCysGlnThrCysGlnAlaArgPheValGln 613  
Db 1266 CGCATTCATTCGGAGAGAAACCTTAAAGTGTAGACGTGCGGCTCGCGCTTGTACAG 1325  
Qy 614 ValAlaHisLeuArgAlaHisValLeuLeHisThrGlnGluLysProTyrProCysGln 633  
Db 1326 GTGGCACTCTCGGGGGGACGTGCTGATCCACCGGGAGAAAGCCTTACCTTGGCCT 1385  
Qy 634 IleCysGlnThrArgPheArghHisLeuGlnThrLeuLysSerHisLeuArgLHisThr 653  
Db 1386 ACCGCGGAAACCCGCTCCGCACTGTGACACCTCAAGAACCAAGTTCGATCCACACC 1445  
Qy 654 GlnGlnLysProTyrHisCysGlnLysCysAsnLeuHisPheArghHisLysSerGlnLeu 673  
Db 1446 GGAAGAAAGCTTACACGTGACCCCTGTGGCTTCCGTCATTCGCGACAAAGTCAACTG 1505  
Qy 674 ArgLeuHisLeuArgGlnLysHisGlnAlaLeHisThrAsnThrLysValGlnTyrArgVal 693  
Db 1506 CGGTCGATCTGGCCCAAGAAACAGAGCTGTCAACCAAGTGCATCACTCACTT 1565

RESULT 10  
US-09-815-379-3  
Sequence 3, Application US/09815379  
Publication No. US2003073613A1  
GENERAL INFORMATION:  
APPLICANT: RASTELLI, LUCA  
APPLICANT: GERRISEN, MARY  
TITLE OF INVENTION: ANGIOGENESIS ASSOCIATED PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE: 10716/35  
CURRENT APPLICATION NUMBER: US/09/815,379  
CURRENT FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 60/191,134  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 1749  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-815-379-3

Alignment Scores:  
Pred. No.: 1,05e-94 Length: 1749  
Score: 1122.50 Matches: 268  
Percent Similarity: 44.1% Conservative: 58  
Best Local Similarity: 36.3% Mismatches: 142  
Query Match: 29.6% Indels: 271  
Gaps: 17  
DB: 3

US-10-755-889-18 (1-706) x US-09-815-379-3 (1-1749)

Qy 1 MetalaserProAla-----AspSerCysIle-----GlnPheThrArgHis 14  
Db 136 ATGGATTCCCGCCCGCCCGAGGAGGAGCGCTGAGTACGTCGGAATTCATCGCCAC 255  
Qy 15 AlaSerAapValLeuLeuAsnLeuAnArgLeuArgSerArgAspIleLeuThrAspVal 34

Db 256 TCCTCCGAGCTGTGGGCAACTCAACGAGCTGCGCTGCGCGGATCTCTCACTGACGTC 315  
Qy 35 ValIleValAlaSerArgGlnGlnPheArgAlaHisLysThrValLeuMetAlaCysSer 54  
Db 316 ACCTGCTGTGGTGGCGGCAACCCCTCAGAGCACACAAAGCAATTCATCTCAGCTGAGT 375  
Qy 55 GlnLeuPheTyrSerLysPheThrAspGlnLeuLysCysAsnLeuValIleAsnLeu 74  
Db 376 GCGCTTCTTCAATCAATTTTCCGGGCGCGCGGAGTCCGGGTGACAGTCTCTCTG 435  
Qy 75 AspProGlnLysLeuAnProGlnGlnLysCysLysLeuLeuAspPheMetTyrThrSerArg 94  
Db 436 CCGGGGGGTCGAGAGGAGGCTTCCGCTTATGTGACTTCACTGACACTTCCGCG 495  
Qy 95 LeuAsnLeuArgGlnGlnLysLeuMetAlaValMetAlaThrAlaMetTyrLeuGlnMet 114  
Db 496 CTGCGCTCTCTCCAGCACTGCAACGAGCTCTAGCGGCGCCACCTTATTTGCAATG 555  
Qy 115 GlnHisValValAspThrCysArgLysPheIleLysAlaSerGlnAlaGlnMetValSer 134  
Db 556 GAGCAGCTGGTCCAGGCATCCACCGCTTATCAGGCCAGC----- 597  
Qy 135 AlaIleLysProProArgGlnGlnPheLeuAsnSerArgMetLeuMetProGlnAspIle 154  
Db 597 ----- 597  
Qy 155 MetAlaTyrArgGlnArgGlnValGlnAsnAsnLeuProLeuArgSerAlaProGln 174  
Db 597 ----- 597  
Qy 175 CysGlnSerArgAlaPheAlaProSerLeuTyrSerGlnLeuSerThrProProAlaSer 194  
Db 597 ----- 597  
Qy 195 TyrSerMetTyrSerHisLeuProValSerSerLeuLeuPheSerAspGlnGlnPheArg 214  
Db 598 -----TGTGAACCTCTGGGCACTCC----- 618  
Qy 215 AspValArgMetProValAlaAsnProPheProLysGlnArgAlaLeuProCysAspSer 234  
Db 618 ----- 618  
Qy 235 AlaArgProValProGlnGlnTyrSerArgProThrLeuGlnValSerProAsnValCys 254  
Db 618 ----- 618  
Qy 255 HisSerAsnLysTyrSerProLysGlnThrIleProGlnGlnAlaArgSerAspMetHis 274  
Db 618 ----- 618  
Qy 275 TyrSerValAlaGlnGlnLysPheProAlaAlaProSerAlaArgAsnAlaProTyrPhe 294  
Db 619 -----CTGCGGCCCTG----- 630  
Qy 295 ProCysAspLysAlaSerLysGlnGlnGlnArgProSerSerGlnAspGlnIleAlaLeu 314  
Db 631 -----GAGCAGAAACCTCCCA----- 648  
Qy 315 HisPheGlnProProAlaAlaProLeuAsnArgLysGlnLeuValSerProGlnSerPro 334  
Db 649 -----CCCCAAGGCCCT-----CCACCAAGTACGTC 678  
Qy 335 GlnLysSerAspCysGlnProAsnSerProThrGlnAlaCysSerSerLysAsnAlaCys 354  
Db 679 AGGCGCTCCAGAGCAACCCAGACCACTGATCTGAGAC----- 723  
Qy 355 IleLeuGlnAlaSerGlnSerProProAlaLysSerProThrAspProLysAlaCysAsn 374  
Db 724 -----TGCAGTCAAGGCCCCCGACGTCAGACGCCCTGACCCCAAGCGCTGCAAC 774  
Qy 375 ThrLysLysTyrLysPheIleValLeuAsnSerLeuAsnGlnAlaLysProGlnLys 394  
Db 775 TGAAGAAAGTCAAGTACATGCTCTAACTCT----- 807

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QY 395 ProGUgluAlaGluLeuGlyArgLeuSerProAlaGlyTyrThrAlaProProAlaCys 414
      ::::: ||||| ::::: |||||
Db 808 ---CAGGCTCCCAAGCAGGAGCTGGTGGGAGAGAAAGTCTGTCAAGCTGGCC 864
QY 415 GlnProMet---GlnProGluAlaLeuAspLeuGlnSerProThrIlySerAla 433
      ||| ::::: ||| ::::: |||
Db 865 CAAGCAGGCTCCCAAGCAGGAGCTGGTGGGAGAGAAAGTCTGTCAAGCTGGCC 924
QY 434 SerGlyGluAspSerThrIlePro---GlnAlaSerArgLeuAspLeuAlaVala 452
      ||| ::::: ||| ::::: |||
Db 925 AGCAGTGAAGAAAGACCCATTCTGTCCCAAGCAGGCTC----- 966
QY 453 SerMetThrGlySerProArgSerSerSerGlnSerHisSerProLeuTyrMetHisPro 472
      ||||| ::::: |||||
Db 967 ---TCTCCAACTGCTGCACGTGCAGTTC----- 993
QY 473 ProLysCysThrSerCysGlySerGlnSerProGlnHisAlaGluMetCysLeuHisThr 492
      ||||| ::::: |||||
Db 994 ---AAATGTGGG-----GCTCCAGCAGTACCCCTACCTCCATCATCC 1035
QY 493 AlaGlyProThrPheAlaGluMetGlyIleThrGlnSerGluTyrSerAspSerSer 512
      ||| ::::: ||| ::::: |||
Db 1036 CAG-----GCTCAAGACACCTGTGATCACCTCTGAACGGGCTCGTCCACTA 1083
QY 513 CysGluAspGlyAlaPhePheCysAspGluCysAspCysArgPheSerGluAlaSer 532
      ||| ::::: ||| ::::: |||
Db 1084 CCGGAGTGAATTTTCAAGTCCAGAACTGTGAGCTGGCAGAGGCTCATCGGG 1143
QY 533 LeuLysArgHisThrLeuGlnThrHisSerAspLysProTyrLysCysAspArgCysGln 552
      ||| ::::: ||| ::::: |||
Db 1144 CTGGAC---TCTTGGTCTCTGGGAGAAAGAAACCAACCTATAAGTGTACGTGTCCGG 1200
QY 553 AlaSerPheArgTyrLysGlyAsnLeuAlaSerHisLysThrValHisThrGlyGlyLys 572
      ::::: ||||| ::::: |||||
Db 1201 TCTTCGTTCCGTAACAAGGCAACTGTGCAGTCACTGACAGTGCACACAGGGGAAAG 1260
QY 573 ProTyrArgCysAspAsnLysCysGlyAlaGlnPheAspArgProAlaAsnLeuLysThrHis 592
      ::::: ||||| ::::: |||||
Db 1261 CCTTACCACTGCTCAATCTGGAGCCGCTTTTAAACCGGCAACAACTGAAAGCGCAC 1320
QY 593 ThrArgIleHisSerGlyGlyLysProTyrLysCysGlyIleThrCysGlyAlaArgPheVal 612
      ::::: ||||| ::::: |||||
Db 1321 AGCGCATTCATTCCGGAAGAAAGCCTATAAGTGTAGACGTGGCTCGCGCTTTGTA 1380
QY 612 ----- 612
Db 1381 CAGGTACGAGCAGCCTCCCAAGTGGCTTCCAAAGCAAACTGCAGAGGTGGGTGGGC 1440
QY 613 -----GlnVal 614
Db 1441 CAAAAGGAGGTTCTGTCTCCCAAGAGCAGAGCTTGAAGTCTCTCCCTCCCAAGGT 1500
QY 615 AlaHisLeuArgAlaHisValLeuLeuHisThrGlyGlyLysProTyrProCysGlyIle 634
      ::::: ||||| ::::: |||||
Db 1501 GCACATTTGGGGGCGACGTGTGATTCACACCGGGAGAAAGCCCTTACCTTCCCTAC 1560
QY 635 CysGlyIleThrArgPheArgHisLeuGlnThrLeuLysSerHisLeuArgIleHisThrGly 654
      ::::: ||||| ::::: |||||
Db 1561 TGGGAAACCGGCTTCGCGCACCTGCAGAACCTCAGAGCAGCAGTTCGATCCACACGGA 1620
QY 655 GlnLysProTyrHisCysGlyLysCysAsnLeuHisPheArgHisLysSerGlnLeuArg 674
      ::::: ||||| ::::: |||||
Db 1621 GAGAAAGCTTACCACTGAGCCCTGTGGCTGTGATTTCCGCAACAAGATCTCAACTGGGG 1680
QY 675 LeuHisLeuArgGlnLysHisGlyAlaIleThrAsnThrIlySerValGlnTyrArgVal 693
      ::::: ||||| ::::: |||||
Db 1681 CTGATCTTGGCCGAAACACGAGTGTCTACCAACCAAAAGTCACTACACATT 1737

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RESULT 11  
 US-10-974-440-92  
 ; Sequence 92, Application US/10974440  
 ; Publication No. US20050214795A1

```

/ GENERAL INFORMATION:
/ APPLICANT: HILLMAN, Jennifer L.
/ APPLICANT: BANDMAN, Olga
/ APPLICANT: LAL, Preeti
/ APPLICANT: YUE, Henry
/ APPLICANT: REDDY, Roopa
/ APPLICANT: TANG, Y. Tom
/ APPLICANT: GERSTIN, Edward H.
/ APPLICANT: ARVIZU, Chandra
/ APPLICANT: BAUGHN, Mariah R.
/ APPLICANT: AZIMZAI, Yalda
/ APPLICANT: LU, Dyrung Aina M.
/ TITLE OF INVENTION: Human Transcriptional Regulator Molecules
/ FILE REFERENCE: PF-0509 USN
/ CURRENT APPLICATION NUMBER: US/10/974,440
/ CURRENT FILING DATE: 2004-10-26
/ PRIOR APPLICATION NUMBER: US/09/674,743
/ PRIOR FILING DATE: 2002-09-23
/ PRIOR APPLICATION NUMBER: PCT/US99/09935
/ PRIOR FILING DATE: 1999-05-04
/ PRIOR APPLICATION NUMBER: 60/084,254
/ PRIOR FILING DATE: 1998-05-04
/ PRIOR APPLICATION NUMBER: 60/095,827
/ PRIOR FILING DATE: 1998-08-07
/ PRIOR APPLICATION NUMBER: 60/102,745
/ PRIOR FILING DATE: 1998-10-02
/ NUMBER OF SEQ ID NOS: 130
/ SOFTWARE: PERL Program
/ SEQ ID NO 92
/ LENGTH: 2741
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No: 1484257CBI
/ US-10-974-440-92

Alignment Scores:
Pred. No.: 2,73e-48 Length: 2741
Score: 630.00 Matches: 208
Percent Similarity: 41.7% Conservative: 104
Best Local Similarity: 27.8% Mismatches: 230
Query Match: 16.6% Indels: 147
DB: 9 Gaps: 26

US-10-755-889-18 (1-706) x US-10-974-440-92 (1-2741)
QY 9 IleglnPheThrArgHisAlaSerAspValLeuLeuAsnLeuAsnArgLeuArgSerArg 28
      ::::: ||||| ::::: |||||
Db 201 ATGGAATTTCCCAAGCAGCAGCAGCATGTCTTGAACAGCTGAACAGCAGGCGAGCTG 260
QY 29 AspIleLeuThrAspValValIleValAlaSerArgGluGlnPheArgAlaHisLysThr 48
      ::::: ||||| ::::: |||||
Db 261 GGGCTTCTCTGTGATGCGACCTTGTGGTGAAGGTGTCACTTAAAGCTCATAAAGCA 320
QY 49 ValLeuMetAlaCysSerGlyLeuPheTyrSerIlePheThrAspGlnLeuLysCysAsn 68
      ||||| ::::: ||||| ::::: |||||
Db 321 GTGGTGGGCGCTTCAGCAGCAAGTACTTCAAGATGCTTGTGTGACCAAG----- 368
QY 69 LeuSerValIleAsnLeuAspProGluIleAsnProGluGlyPheCysIleLeuLeuAsp 88
      ::::: ||||| ::::: |||||
Db 369 AAGGAGTGTGTGACCTGACATCACT---AACGGCGAGGCGCTGGGCGAGGTGTGAG 425
QY 89 PheMetTyrThrSerArgLeuAsnLeuArgGluGlyAsnIleMetAlaValMetAlaThr 108
      ::::: ||||| ::::: |||||
Db 426 TTTATGTACACGGCAGCAGTGTAGCCCTGAGCCCTGAGAAAGAGATGATGTGTGGCGGTG 485
QY 109 AlaMetTyrLeuGluMetGluHisValAlaAspThrCysArgLysPheIleLysAlaSer 128
      ::::: ||||| ::::: |||||
Db 486 GCCACTTCTCCAAATGCAAGACATCATCAGGCTGCCAT----- 527
QY 129 GluAlaGluMetValSerAlaIleLysProArgGluGluPheLeuAsnSerArgMet 148
      ::::: |||||

```





Db 1660 CGGCCCTCTAAGTCCGAGAGTGTGGAGACATTACACACTTCAGGAGACCTGAGCG 1719  
 QY 535 GHIETHTLEUGINTHTHISER---ASPLYSPROYLYSCYASAPARYCYGGINALASE 554  
 Db 1720 GCAC---CTTGCGATCCACAGCGGGAGAGACCTTACGTGTGCATCCACTCCAGCGACA 1776  
 QY 554 rPhearGTyrlrsglyanleuAlaserHlsyThrvAlHlsThrglyulysProTy 574  
 Db 1777 GTTTCAGACACCCGCGCTCTGACAGCGGACGTCGCGCATTCACAGGTGAGAACCCATG 1836  
 QY 574 rArgCYsAnlleCYsGlyAlaGlnPhesAnrProAlaAnleuLySTHrHlsThrAr 594  
 Db 1837 CCAETGTGTATGTGCGGTAAAGCCTTACACCAAGCCAGCTCCCTCATCCGCCACGTGCG 1896  
 QY 594 gIhIsSerGlyulysProTyLySCySglnThrCYsGlyAlaArGpHeValGlnVa 614  
 Db 1897 CCAGACACCGGGAGAGACCTTACGTGCGAGCGCTGCGCAAGAGATTCGTCCAGTTC 1956  
 QY 614 lAlaHlsleuArGAlaHlsValleuHlsThrGlyulysProTyrrProCYsGlnI 634  
 Db 1957 CAGCCAGTGGCCATCATTCATTCGCCACACGACAAACATCCGCCACCAAGTGCAGCGT 2016  
 QY 634 eCYeGlyThrArGpHeArGHIleuGlnThrleuLySerHlsleuArGlyHlsThrG 654  
 Db 2017 GTGCAGCAGGCTTCGTGAAAGTGGGAGCCTGTCCAGACATCATTCATTCACACTCG 2076  
 QY 654 YGlylySProyThrHlsCYsGlyulysCYsAnlleuHlsPhesArGHIlsySerGlnLeuAr 674  
 Db 2077 AGAGAGGCTTACCTGTGTATAGTGTGGGTGCGCTTCAACCGGATGAGCAACCTGCG 2136  
 QY 674 gLeuHlsleuArGlnlySHlsGlyAlaHlsThrAnThrlySValGlnTyrrArGValSe 694  
 Db 2137 CTCCACGCTGAGACCGTGCACACAGGCGACAGGCGATCAAGATC----- 2182  
 QY 694 rAlaThraspleuProProGln 701  
 Db 2183 -----CTGAGGCCCGAG 2194

## RESULT 13

US-10-117-722-309

Sequence 309, Application US/10117722

Publication No. US20030219744A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Dmanac, Radoje T.

TITLE OF INVENTION: No. US20030219744A1 Nucleic Acids and

FILE REFERENCE: Polypeptides

CURRENT APPLICATION NUMBER: US/10/117,722

CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: 09/620,312

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1104

SOFTWARE: pc\_fl\_genes Version 1.0

SEQ ID NO 309

LENGTH: 2769

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (248) ..(2659)

US-10-117-722-309.

Alignment Scores:

Pred. No.: 1,74e-47

Length: 2769

Matches: 205

Percent Similarity: 41.0%  
 Best Local Similarity: 27.4%  
 Query Match: 16.4%  
 DB: 6  
 US-10-755-889-18 (1-706) x US-10-117-722-309 (1-2769)

QY 9 lIeGlnPhesThrArGHIlsAlaserAspValleuAnleuAnArGleuArGSerArg 28  
 Db 248 ATGACACTTCCCGACAGACAGCATGTCTTGAAACAGCTGAACCGACGCGACACTG 307  
 QY 29 AspIleuThrArpValValleValSerArgGlnGlnPhesArGAlaHlsyThr 48  
 Db 308 GCGCTTCTGTGATCCTACCTTGTGTGTGAGCGTTCCTACTTAAGGCTCATAAAGCA 367  
 QY 49 ValIeueArGlySerGlyleuPherTySerIlePhesThrArpGlnleuLySCyAsn 68  
 Db 368 GTGCTGGCGGCTGACAGAGTACTTCAGATGTCCTTGTGTGACAG----- 415  
 QY 69 leuSerValIleAnleuAspProGlnIleAnProGlnGlyPheCySileleuLeuAsp 88  
 Db 416 AAGGACGTGTGACCTGACATCATG---AAGCGGACAGCCTGGGCGACGCTGAG 472  
 QY 89 PheMetTyrrThrSerArGleuAnleuArGlyulysAnlleuArGAlaValMetAlaThr 108  
 Db 473 TTATGTACACGCGCAAGCTGAGCTGAGCTGAGACCTGAGAACGTGATGTCTGCGCGTG 532  
 QY 109 AlameTyrrleuGlnMetGlnHlsValAlaArPhrCYsArGlySPheIleValSer 128  
 Db 533 GCCACTTCCCTCCAAATGACAGACATCATCGGCGCTGCATGCTCAAGTCACTTGC 592  
 QY 129 GluAlaGlnMetValSerAlaIlelySProyProArGlnGlnGlnPheleuAnSerArgMet 148  
 Db 593 GAG-----CCGCTACCGAGCCT----- 610  
 QY 149 leuMetProGlnIleMetAlaTyrrArGlyArGlnValValGluAnAsnleuPro 168  
 Db 611 -----GGGGAAGATCCGAG 625  
 QY 169 leuArGSerAlaProGlyCYsGlySerArGAla-----PheAlaProSerleu 184  
 Db 626 GCGTTGGCGACAGAGGAGGAGACAGAGCCAAAGAGAGAGTGGCCACGACGAG 685  
 QY 185 TyrrSer-----GlyleuSerThrPro-----ProAlaSerTyrrSerMet 197  
 Db 686 CTGAGCAGGCTGAGCAGGCGAGGACGACACCTATAGCCGCCAG----- 733  
 QY 198 TyrrSerHlsleuProValSerSerleuLeuPheSerArpGlnGlnPheArGValArg 217  
 Db 734 -----AGGACCTCAAG 745  
 QY 218 MetProValAlaAnProPheProlyGlnArGAlaLeuProCYsAspSerAlaArgPro 237  
 Db 746 -----GAGAGGCGGCGGTGAGGCCAGAGTGGCGGCGAGC 781  
 QY 238 ValProGlyGlnTyrrSerArgProThrleuGlnValSerProAnValCYsHlsSerAn 257  
 Db 782 GGTCCAGACAGACAGAGAACCGCAT----- 808  
 QY 258 lIeTyrrSerProlySGlyulThrIleProGlnGlnAlaArgSerArpMetHlsTyrrSerVal 277  
 Db 809 -----GCGCCCGAGGCGCGCGCTGTGAGCTCAAGCCACACCCACAGTGGCATG 862  
 QY 278 AlaglnGlyleuLySProyAlaAlaProSerAlaArgAnAlaProTyrrPheProCYsAsp 297  
 Db 863 GCTGCGCGAGAGGTAGGCGCGCTTGTCCGAGAGCTCGAGCAAGAAATGAGGTGAG 922  
 QY 298 LysAlaSerlySGlnGlnGlnArGProSerSerGlnAspGlnIleAlaHlsPheGln 317  
 Db 923 CCGCGCGGAGAGGAGAGAGCAAAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 982  
 QY 318 ProProAnAlaProleuAnArGlyGly-----leuValSerProGlnSerProGln 335

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Db 983 GGCGCA---GCTGAGGTCAAGAGAGAGGTTCCAGCTGGAGAACGAGAGGCCCGCCGAG 1039
Qy 336 LysSerAspCysGlnProAsnSerProThr-----GluAlaCysSerSer-Ly 351
Db 1040 GAAAGACGAGATATGAGGATCAGCGGCGACAGACTCGGGGAGAGAGCTCGGCTCGAGGCC 1099
Qy 351 aaanaLaCysAlaLeuGlnAlaSerGlySerProAlaLysSerProThrAspProLy 371
Db 1100 CGGGGCTGCTGCTCAGGACCTTACGGGACCGGACCGGACCTTACGGCTCCGCTC 1159
Qy 371 baLaCysAsnTrpLysLysTrpLysPheLeuValLeuAsnSerLeuAsnGlnAlaLys 391
Db 1160 ATCCAGACAGTGCAGAG-----ACTGTGGAGAGAGGTTCCAGCACGCGGGAAC 1207
Qy 391 sProGlyGlyProGlnGlnAlaGluLeuGlyArgLeuSerProArgAlaTrpThrAla-- 410
Db 1208 TTCAGAGCGACATCCGATCCACACGCGGAGAGAGCCCTTCTGTGTCGCGGAGTCCAGC 1267
Qy 411 ----ProProAlaCysGlnProProMetGluPro-----GluAsnLeuAspLeuGlnSe 427
Db 1268 AAGGCTTTTCCAGCCCGGCGCGTGCAGAGCCCATGAGAGAGACAGCAGCCCTCGAAG 1327
Qy 427 rProThrLysLeuSerAlaSerGlyLysAspSerThrLeProGlnAlaSerArgLeuAs 447
Db 1328 CCTTACCGCTGCGAGAGTGCAGGAGAGAGCTACC-----GCCCTCATCAGGCTTG 1375
Qy 447 naenilleValAsnAspSerMetThrGlySerProArgSerSerSerGlnSerHisSerP 467
Db 1376 CTGAACCTGCACAAAGAGCGGCACTCGGCGAGGCGGCTACCGCT--GCGAGAGCTGC 1432
Qy 467 oLeuTrpMetHisProProLysCysThrSer-----CysGlySerGly 481
Db 1433 GCGAAGCTCTTCCACCACTCGGCGAAGCTTCAAGGCGCACAGCTGTGCGACAGCGGAG 1492
Qy 481 nSerProGlnHisAlaGluMetCysLeuHisThrAlaGlyProThrPheAlaGlu---- 499
Db 1493 AAGCCCTTAC-CAGTGCAGTACTATGC-----GGCGGCTCTTCTCCAGCCCGAC 1539
Qy 500 -----GluMetGlyGluThrGlnSerGlyTrpSerAspSerSerC 513
Db 1540 TTCAGAGTGCAGCCAGCTGGAGACCCAGACGAGACAGAGACAAAGTCCACACTG 1599
Qy 513 sGlu-----As 515
Db 1600 CGACAAAGATTCAACAGAGTGAAGGAACCTGAAGGCCCTGAAGATCCACATCGCTGA 1659
Qy 515 nglyAlaPhePheCysAsnGluCysAspCysArgPheSerGlnGlnAlaSerLeuLysAr 535
Db 1660 CGGGCCCTTCAAGTGCAGAGTGTGGAGAGAGTTCAACCACTCAAGGAAACCTGAAGCG 1719
Qy 535 gHisThrLeuGlnThrHisSer---AspLysProTrpLysCysAspArgCysGlnAlaSe 554
Db 1720 GCAC---CTTCGAGTCCACAGCGGGGAGAGCCCTTACGTGTGATCCACATCGCCAGCACA 1776
Qy 554 rPheArgTrpLysGlyAsnLeuAlaSerHisLysThrValHisThrGlyGluLysProTy 574
Db 1777 GTTTGACAGACCCCGGCGCTCTGCAGCGGCACTCCGATTCACACAGATGAAGAGCAGT 1836
Qy 574 rArgCysAsnLLeCysGlyAlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrAr 594
Db 1837 CCAAGTGTGTATGTGGGTAAAGGCTTACCCAGGACGACTCCCTCATTCGCCACGTCGGC 1896
Qy 594 gLleHisSerGlyGluLysProTrpLysCysGlnThrCysGlyAlaLysPheValGlnVa 614
Db 1897 CCAGACACACCGGAGAGAGCCCTTACGTGAGACGCTGCGGCAAGAGATTTCGCCAGTC 1956
Qy 614 lAlaHisLeuArgAlaHisValLeuLleHisThrGlyGluLysProTrpCysGlyLui 634
Db 1957 CAGCAGTGGCCATCATATTCGCCACACAGACAAACATCGCCACACAAAGTGCAGAGT 2016
Qy 634 eCysGlyThrArgPheArgHisLeuGlnThrLeuLysSerHisLeuArgLleHisThrGl 654
Db 2017 GTGCAGCAAGGCTTCTCGTGAACGTGGGGAAGCTGTCCAAAGACATCATTCACACTGG 2076

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Qy 654 yGluLysProTrpLysCysGlyLysCysAsnLeuHisPheArgHisLysSerGlnLeuAr 674
Db 2077 AAGAGAGCTTTCCTGTGTGATGATGTGGCGGTGCTTCAACCGGGATAGACAACTGGC 2136
Qy 674 gLeuHisLeuArgGlnLysHisGlyAlaLleThrAsnThrLysValGlnTrpArgValSe 694
Db 2137 CTCACAGCGAGAGACCGGTGCACAGGAGGAGGAGGAGGAGCATCAAGATC----- 2182
Qy 694 rAlaThrAspLeuProProGlu 701
Db 2183 -----CTGAGACCCGAG 2194

RESULT 14
US-10-122-851-309
/ Sequence 309, Application US/10122851
/ Publication No. US20050239060A1
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Ren, Feiyang
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: Novel Nucleic Acids and
/ FILE REFERENCE: 784CIP2BDV3
/ CURRENT APPLICATION NUMBER: US/10/122,851
/ PRIOR FILING DATE: 2002-04-12
/ PRIOR APPLICATION NUMBER: 09/620,312
/ PRIOR FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: 09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: 09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ NUMBER OF SEQ ID NOS: 1104
/ SOFTWARE: pc_fl_genes version 1.0
/ SEQ ID NO 309
/ LENGTH: 2769
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (248)..(2659)
US-10-122-851-309

Alignment Scores:
Pred. No.: 1,74e-47 Length: 2769
Score: 621.50 Matches: 205
Percent Similarity: 41.0% Conservative: 102
Best Local Similarity: 27.4% Mismatches: 288
Query Match: 16.4% Indels: 154
DB: 9 Gaps: 25

US-10-755-889-18 (1-706) x US-10-122-851-309 (1-2769)
Qy 9 lLeGlnPheThrArgHisAlaSerAspValLeuLeuAsnLeuAsnArgLeuArgSerArg 28
Db 248 ATGAGATTTTCCCGACAGACAGCAGCATGTCTTGAACACACTGAACAGACAGAGCGTGG 307
Qy 29 AspLleLeuThrAspValValleValAlaSerArgGluGlnPheArgAlaHisLysThr 48
Db 308 GGGCTTCTGTGATCGACACTTGTGTGTGACGCGTTCACCTTAAAGCTCTTAAGACA 367
Qy 49 ValLeuMetAlaCysSerGlyLeuPheTrpSerLlePheThrAspGlnLeuLysCysAsn 68
Db 368 GTGCTGCGCGCTGACGAGAGTACTTCAAGATGCTTGTGTGACAG----- 415
Qy 69 LeuSerValLleAsnLeuAspProGluLleAsnProGluGlyPheCysLleLeuLeuAsp 88
Db 416 AAGAGATGTGTGACCTTGACATCACT---AACGCGGAGGCTGCGGAGGAGTGTGAG 472
Qy 89 PheMetTrpThrSerArgLeuAsnLeuArgGluGlyAsnLleMetAlaValMetAlaThr 108

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Db 473 TTTATGTACAGCGGCAAGCTGAGCCCTGAGAGCCCTGAGATGATGTCCTGCGCTG 532  
 Qy 109 A1aMetTyrLeuGlnMetGlnHisValValAAspThrCysArgLysPheIleLysAlaSer 128  
 Db 533 GCGACTTTCCTCCGAATGCAAGACATCATCAGCGCTGCGCATGCGCTCAAGATCATTGCT 592  
 Qy 129 G1uAlaGlnMetValSerAlaIleLysProProArgGlnGlnPheLeuAsnSerArgMet 148  
 Db 593 GAG-----CCGGCTACCAAGCCCT----- 610  
 Qy 149 LeuMetProGlnAspIleMetAlaTyrArgGlnValValGluAsnAsnLeuPro 168  
 Db 611 -----GGGGAAATGCGGAG 625  
 Qy 169 LeuArgSerAlaProGlnCysGlnSerArgAla-----PheAlaProSerLeu 184  
 Db 626 GCGTTGGCGCAAGAGAGGAGGAGACAGAGGCCAAAGAGAGAGAGTGGCCACAGCGAG 685  
 Qy 185 TyrSer-----GlyLeuSerThrPro-----ProAlaSerTyrSerMet 197  
 Db 686 CTGAGCAGGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 733  
 Qy 198 TyrSerHisLeuProValSerSerLeuLeuPheSerAspGlnGlnPheArgAspValArg 217  
 Db 734 -----AGGAGACTTCAG 745  
 Qy 218 MetProValAlaAsnProPheProLysGlnArgAlaLeuProCysAspSerAlaArgPro 237  
 Db 746 -----GAGAGCGCGCGCGCTGAGCGCCCGCAAGTGGCGCGCAGC 781  
 Qy 238 ValProGlnGlnTyrSerArgProThrLeuGlnValSerProAsnValCysHisSerAsn 257  
 Db 782 GGTCCAGACGACAGAGAGAAAGCCGAT----- 808  
 Qy 258 IleTyrSerProLysGlnThrIleProGlnGlnAlaArgSerAspMetHisTyrSerVal 277  
 Db 809 -----GGCGCCCGGAGCGCGCGCTGTGAGCTCAAGCCAGCCAGCCAGAGTGGCATG 862  
 Qy 278 AlaGlnGlnLeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAsp 297  
 Db 863 GCTGCGCGCAAGCTGAGGCGCGCTTGTCCAGAGCTGCGAGCAAGAAATGAGGTGAG 922  
 Qy 298 LysAlaSerLysGlnGlnArgProSerSerGlnAspGlnIleAlaLeuHisPheGln 317  
 Db 923 CCGCGCGGAAAGGAGGAGAGAGCAAAAGAGCAAGAGCAAGAGAGAGAGGCGCGCA 982  
 Qy 318 ProProAsnAlaProLeuAsnArgLysGly-----LeuValSerProGlnSerProGln 335  
 Db 983 GGGCCA---GCTGAGGTCAAGAGAGAGGAGGTTCACAGCTGAGAGAACGAGAGGCGCGCAG 1039  
 Qy 336 LysSerAspCysGlnProAsnSerProThr-----GluAlaCysSerSer-Ly 351  
 Db 1040 GAGAAACGAGAAATGAGAGACTCAAGCGGCGCAACACTGGGCGAGAGCTGGCTCCAGAGCC 1099  
 Qy 351 AsnAlaCysLysIleLeuGlnAlaSerGlySerProProAlaLysSerProThrAspProLys 371  
 Db 1100 CGGGCGCTTCGCTCAAGGACCTCAAGGCGAGCGAGAGAGTCCAAAGCGCTCAAGCGCTCG 1159  
 Qy 371 AlaCysAsnTrrLysLysTyrLysPheIleValLeuAsnSerLysLeuAsnGlnAsnAlaLys 391  
 Db 1160 ATCCACAAGTCCGAGG-----ACTGTGGAGAGAGAGTTCACGCAACGCGGGAAC 1207  
 Qy 391 AspGlnLysGlnAlaGlnAlaGlnLeuGlnLysArgLeuSerProArgAlaTyrThrAla-- 410  
 Db 1208 TTCAGCGGCGACATCCGATCCACACCGGGGAGAAAGCCCTTCTGTCGGGAGAGTGCAC 1267  
 Qy 411 ---ProProAlaCysGlnProProMetGlnPro-----GluAsnLeuAspLeuGlnSer 427  
 Db 1268 AAGGCGCTTTCGAGCCCGCGCTGACAGGCGCCATGAGAGAACGCAACGCGCTTCAGAG 1327  
 Qy 427 ProThrLysLeuSerAlaSerGlnGlnAspSerThrIleProGlnAlaSerArgLeuAs 447  
 Db 1328 CCTATGCGCTGCGAGAGAGTGGGAGAGAGACTAC-----GCTCATCAAGCTTG 1375

Qy 447 nAsnIleValAsnArgSerMetThrGlySerProArgSerSerGlnSerHisSerPr 467  
 Db 1376 CTGAACTTCGACAAAGAGCGGCACTGGGAGAGCGGCTACCGCT---GCGAGACTGC 1432  
 Qy 467 OleuTyrMetHisProProLysCysThrSer-----CysGlySerGln 481  
 Db 1433 GCGAAGCTTTCACACACCTCGGCGAACCTCAAGCGGCAACGAGCTGGTGCACAGCGGAG 1492  
 Qy 481 nSerProGlnHisAlaGlnMetCysLeuHisThrAlaGlyProThrPheAlaGln----- 499  
 Db 1493 AAGCCCTAC-CAGTGGCACTACTGC-----GGCGGCTCTCTTCCGACCCAC 1539  
 Qy 500 -----GluMetGlnGlnThrGlnSerGlnTyrSerAspSerSerCys 513  
 Db 1540 TTCGAAATGCGCCACCTGAGAGCCACGACAGCGAGACAGAGACAGACAGTGGCCACACTG 1559  
 Qy 513 sGlu-----As 515  
 Db 1600 CGACAAAGATTCAACAGGATAGGAACCTGAAGGCCCACTGAATCCATTCAGTGGTGA 1659  
 Qy 515 nGlyAlaPhePheCysAsnGlnCysAspCysArgPheSerGlnGlnAlaSerLeuLysArg 535  
 Db 1660 CGGGCGCTCAAGTGGCGAGAGTGTGGAGAGCACTTCAACACCTCAGGGAACCTGAAGCG 1719  
 Qy 535 GHisThrLeuGlnThrHisSer---AspLysProTyrLysCysAspArgCysGlnAlaSer 554  
 Db 1720 GCAC---CTTCGGATCCACAGCGGAGAGAGCCCTTACGTGTGATCCATCCAGCGACACA 1776  
 Qy 554 rPheArgTyrLysGlnValAsnLeuAlaSerHisLysThrValHisThrGlnGlnLysProTyr 574  
 Db 1777 GTTTCGAGACCCCGCGCGCTGTGACGCGGACAGCGGCACTCCGATTCACACAGTGAAGAGCATG 1836  
 Qy 574 rArgCysAsnIleCysGlyAlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArg 594  
 Db 1837 CCACTGTGTATGTGGCGTAAAGGCTTCAACAGGAGCAGCTCCCTCATCCGCCACGTGCG 1896  
 Qy 594 gLeuHisSerGlnGlnLysProTyrLysCysGlnThrCysGlnAlaArgPheValGlnVal 614  
 Db 1897 CCAGCAGACCGGAGAGAGAGCCCTTACGTGTGAGAGCGCTGGCGGAGAGATTCGTCAGATC 1956  
 Qy 614 lAlaHisLeuAlaArgAlaHisValLeuIleHisThrGlnGlnLysProTyrProCysGlnIle 634  
 Db 1957 CAGCAGCTGGCCCAATATATTCGCCCAACAGACAAATCCGCCCAACAAAGTGCAGCT 2016  
 Qy 634 eCysGlyThrArgPheArgHisLeuGlnThrLeuLysSerHisLeuArgIleHisThrGln 654  
 Db 2017 CTGCAGCAAGCGCTTCGTGAACCGTGGGAGCACTGTCCAAAGCAATCATTCACACTGG 2076  
 Qy 654 yGlnLysProTyrHisCysGlnLysCysAsnLeuHisPheArgHisLysSerGlnLeuArg 674  
 Db 2077 AGAAGACCTTACCTGTGTGATGATGTGGCGGTGCTCAACCGGATGAGCAACCTGGCG 2136  
 Qy 674 gLeuHisLeuAlaArgGlnLysHisLysValAlaIleThrAsnThrLysValGlnTyrArgValSer 694  
 Db 2137 CTCCAGGTGAAGACCTGTGACAGGCGCAAGGCGCAAGGCAATCAATCAAGATC----- 2182  
 Qy 694 rAlaThrAspLeuProGln 701  
 Db 2183 -----CTGAGAGCCCGAG 2194  
 Db 2194

RESULT 15  
 US-10-486-977-45  
 ; Sequence 45, Application US/10486977  
 ; Publication No. US20050123912A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCTE CORPORATION; BAROSSO, Ines;  
 ; APPLICANT: BAUGHN, Mariah R.; BECHA, Shanya D.;  
 ; APPLICANT: BLAKE, Julie J.; BOROMSKY, Mark L.;  
 ; APPLICANT: BURFORD, Neil; DUGGAN, Brendan M.;  
 ; APPLICANT: ELIJOTT, Vicki S.; EMERLING, Brooke M.;  
 ; APPLICANT: FORSYTHE, Ian J.; GIETZEN, Kimberley J.;  
 ; APPLICANT: GORVAD, Ann E.; GRIFFIN, Jennifer A.;

APPLICANT: HAFALIA, April J.A.; HONGHELI, Cynthia D.;  
APPLICANT: ISON, Craig H.; KHAN, Farrah A.;  
APPLICANT: LAL, Preeti G.; LEE, Ernestine A.;  
APPLICANT: LEE, Sally; LEE, Soo Yeun;  
APPLICANT: LI, Joana X.; LU, Dying Aina M.;  
APPLICANT: LU, Joan; LEHR-MASON, Patricia M.;  
APPLICANT: NGUYEN, Daniel B.; RAMKUMAR, Jayalaxmi;  
APPLICANT: SPRAGUE, William W.; TANG, Y. Tom;  
APPLICANT: THANGAVELU, Kavitha; THORNTON, Michael B.;  
APPLICANT: TRAN,uyen K.; CHAMLA, Narinder K.;  
APPLICANT: WARREN, Bridget A.; XU, Yuming;  
APPLICANT: YAO, Monique G.; YUE, Henry;  
APPLICANT: YUE, Hubbin; ZEBARJADIAN, Yeganeh  
TITLE OF INVENTION: NUCLEIC-ACID ASSOCIATED PROTEINS  
FILE REFERENCE: PF-1146 USN  
CURRENT APPLICATION NUMBER: US/10/486, 977  
CURRENT FILING DATE: 2004-02-17  
PRIOR APPLICATION NUMBER: PCT/US02/25829  
PRIOR FILING DATE: 2002-08-14  
PRIOR APPLICATION NUMBER: US 60/313,111  
PRIOR FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/314,682  
PRIOR FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/314,756  
PRIOR FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/315,105  
PRIOR FILING DATE: 2001-08-27  
PRIOR APPLICATION NUMBER: US 60/316,751  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/316,856  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/328,185  
PRIOR FILING DATE: 2001-10-05  
NUMBER OF SEQ. ID NOS: 66  
SOFTWARE: PERL Program  
SEQ. ID NO 45  
LENGTH: 3451  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: incycle ID No: 3217430CB1  
US-10-486-977-45  
  
Alignment Scores:  
Pred. No.: 2,996-42 Length: 3451  
Score: 567.00 Matches: 199  
Percent Similarity: 39.1% Conservative: 95  
Best Local Similarity: 26.5% Mismatches: 243  
Query Match: 14.9% Indels: 215  
Gaps: 26  
US-10-755-889-18 (1-706) x US-10-486-977-45 (1-3451)  
QY 14 HislaserpValleuleuAenleuAnArgSerArgAepIleLeuThrAsp 33  
DB 150 CACGCGCCATCTGCTCCAGCACTGCATGACGAGCAATCCAGCCGCTTTGGAC 209  
QY 34 ValValleValValSerArgGluGlnPheArgAlaHisLysThrValIleuMetAlaCys 53  
DB 210 TGTATGTGGGTGAAGAGAGCTGCTTTAAAGCCATTAAGATGCTGGCAGCATTC 269  
QY 54 SerGlyLeuPheTyrSerIlePheThrAspGlnLeuLysCysAsnLeuSerValIleAsn 73  
DB 270 AGCAGATATTTCAGACCTCTTTCAGAAATCTTCAAGCAAGAAATGATGTTTTTCAC 329  
QY 74 LeuAspProGluIleAsnProGluGlyPheCysIleLeuLeuAspPheMetTyrThrSer 93  
DB 330 TTGATGTATAA---AATGTCAGTGCATAGGAGAGATCCTGACCTTCATATACATTC 386  
QY 94 ArgLeuAsnLeuArgGluGlyAsnIleMetAlaValMetAlaThrAlaMetTyrLeuGln 113  
DB 387 CATCTAGATCTTAACGACGACAAATATATACAGTAATGCTGGACACAGCAGATGTTTCA 446

QY 114 MetGluHisValValAspThrCysArgLysPheIleLysAlaSerGluAlaGluMetVal 133  
DB 447 GTTCAAAATGTTCTAGCTGTGTGCACACATTTTAAATATACAGC----- 491  
QY 134 SerAlaIleLysProProArgGluGlnPheLeuAsnSerArgMetLeuMetProGluAsp 153  
DB 492 ACTGTAATGACAGCCACTGGC-----ATGGCT----- 518  
QY 154 IleMetAlaTyrArgGlyArgGluValValGluAsnAsnLeuProLeuArgSerAlaPro 173  
DB 518 ----- 518  
QY 174 GlyCysGluSerArgAlaPheAlaProSerLeuTyrSerGlyLeuSerThrProAla 193  
DB 519 ---TGTATATGACATTC-----TCTCAACAAAGACCCCTG---ACCCAGATGCC 563  
QY 194 SerTyrSerMetTyrSerHisLeuProValSerSerLeuLeu---PheSerAspGluGlu 212  
DB 564 ACTTGATGATACAGTGAAGAACTACCCCTCATTTACTGCAGGAATGTTTCAGCAGATGCA 623  
QY 213 PheArgAspValArgMetProValAlaAsnProPheProLysGluArgAlaLeuProCys 232  
DB 624 CAGCAGAAACAAACGTTGATGATGCAATCGATCCG-----CATGCTTCACCATCA 671  
QY 233 AspSerAlaArgProValProGlyLysTyrSerArgProThrLeuGluValSerProAsn 252  
DB 672 GTTATTCGCATCACTCCGACAGTGAATCTCAAAACAGCCTCGATATCTTCAGATGCG 731  
QY 253 ValCysHisSerAsnIleTyrSerProLysGluThrIleProGluGluAlaArgSerAsp 272  
DB 732 ACCTGC-----ACAGAACTGCTTTCAAA---CAGCCAAT 764  
QY 273 MetHisTyrSerValAlaGluGlyLeuLysProAlaAlaProSerAlaArgAsnAlaPro 292  
DB 765 TACTATTCACAACTC-----AGAAAC----- 785  
QY 293 TyrPheProCysAspValAserLysArgGluGluArgProSerSerGlyAspGluIle 312  
DB 786 ---TTTACAGTAAGACAGTACCATTAACACGAGCTGCTCCAGTCAGAGAGAGTGT 842  
QY 313 AlaLeuHisPheGluProProAsnAlaProLeuAsnArgLysGlyLeuValSerProGln 332  
DB 843 -----GAGAGCCTTTGCTTTCAGACACTCTACAGACTTACCAAGCTAGAG 890  
QY 333 SerProGlnLysSerAspCysGlnProAsnSerProThrGluAlaCysSer---SerLys 351  
DB 891 AGC-----CAGCT-----TGCTGTCACTCAT 914  
QY 352 AsnAlaCysIleLeuGlnAlaSerGlySerProProAlaLysSerProThrAspProLys 371  
DB 915 TCTGAATGATCTCTGAGTCT-----CCGAGCAGCTTACCTTCC----- 953  
QY 372 AlaCysAsnTrpLysTyrLysPheIleValLeuAsnSerLeuAsnGlnAsnAlaLys 391  
DB 954 -----AACTTCCTGCGCCAGCCTGTGAAT 977  
QY 392 ProGlyGlyProGluGlnAlaGluLeuGlyArgLeuSerProArgAlaTyrThrAlaPro 411  
DB 978 GACTTGCCCAACACCT-----GAGTCAGAC 1004  
QY 412 ProAlaCysGlnProProMetGluProGluAsnLeuAspLeuGlnSerProThrLysLeu 431  
DB 1005 GCCACATGCCAACACCTGTCAAG-----CAGATGAGGCTCAAAAG 1046  
QY 432 SerAlaSerGlyGluAspSerThrIleProGlnAlaSerArgLeuAsnAsnIleValAsn 451  
DB 1047 GCCAT-TCATCTGAAGAAGCTCAATTCTGTAAGTACAGAAATACGC----- 1093  
QY 452 ArgSerMetThrGlySerProArgSerSer-SerGluSerHisSerProLeuTyrMetHis 471  
DB 1094 -----AGAGCAAGTATCTGAA----- 1109



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QY 471 sProProlyserCysThrSerCysGlySerGlnSerProGlnHisAlaGluMetCysLeuH1 491
    |||||
Db 1110 -----CCCAAG-----TCAGATGATGCTTTGACAAAAGAGTTGA 1144
QY 491 sThrAlaGlyProThrPheAlaGluGluMetGlyGluThrGlnSerGluTyrSerAspSe 511
    |||||
Db 1145 ATCTGCTAGTAAATAATCCCTAGAGAAAGCTAGACAGCCAAAGTCTGTAAGAAAAGAAAG 1204
QY 511 r-----SerCysGluAenGlyAlaPhePheCysAenGluCysAspCysArgPh 527
    |||||
Db 1205 TGAAGAGTGTGTGCTGTTGTGAAT-----TTTAATTGCATTAGTAGAGAGAGAGGCC 1258
QY 527 eSerGluGluAlaSerLeuYsArgHisThrLeuGlnThrHisSerAspYsProTyrLy 547
    |||||
Db 1259 TGAAGACCCGCTGCTCCGTAAGACCAAGTCCAGACACTTCAGTCCAGAGACAAATAGC 1318
QY 547 sCyAspArgCysGlnAlaSerPheArgTyrLyGlyAsnLeuAlaSerHisLySThrVa 567
    |||||
Db 1319 GTGTGAATTATGCGGAAACCTTTTAAACACCCAAAGCACTTGAGAGCTTCACAAAGGTC 1378
QY 567 lHisThrGlyGlyLysProTyrArgCysAsnHisCysGlyAlaGlnPheAsnArgProAl 587
    |||||
Db 1379 TCATACAGGTGAGAAACCTTTTGAATGTAACTTTGTGGAAACATTTCTCTCAGGACAG 1438
QY 587 aAsnLeuYsThrHisThrArgGlyLeHisSerGlyGlyLysProTyrLySArgLutThrCy 607
    |||||
Db 1439 TAACTTCAGACTCAGCTTACAGCGGCATTTCTGTGAAMAAACATATCATCTCGAGATCTG 1498
QY 607 sGlyAlaArgPheValGlnValAlaHisLeuAlaHisValLeuLeuHisThrGlyGly 627
    |||||
Db 1499 TGGAAAGGTTTCAGCTCTGCGAGCTCAGCGTCACTTATATTCCTCAGAGAGA 1558
QY 627 uLyProTyrProCysGluLeuLeuCysGlyThrArgPheArgHisLeuGlnThrLeuYsSe 647
    |||||
Db 1559 AAAACACACTTGTGTGACATCTGTGTGCGAGGTTTAGTAACCTTCAGTAATTGAAAGA 1618
QY 647 r----- 647
Db 1619 GCACAAAAGACACACAGCTGTATAAAGCTTCACCTGTGATGATGTGGAAGTCTTT 1678
QY 647 ----- 647
Db 1679 TAAATATGCAAGAAAGATTAGTAAAGCACAGAAATTCGSCACAGGGGAGCGGCTTACAG 1738
QY 648 -----HisLeuArg11 651
    |||||
Db 1739 CTGCTTCGCTGCGGGAATGTTTGGGGGATCAGGTGACCTCCGACAGGCATGTCCGCAC 1798
QY 651 eHisThrGlyGlyLysProTyrHisCysGlyLysCysAenLeuHisPheArgHisLySSe 671
    |||||
Db 1799 TCACACTGGGAGAAAGCCGTACATGTGAGATCTGTAAACAAGTCTTACCCGCTGTC 1858
QY 671 rGlnLeuArgLeuHisLeuArgGlnLysHisGlyAla-1LeThrAsnThrLysValGlnT 691
    |||||
Db 1859 GGTGCTCCGGCGGCGCAAGAAAGATGCACCTGCAAAAGCTGTGACGAGAGCCAGATGCT 1918
QY 691 yArgValSerAlaThrAspLeuProPro 700
    |||||
Db 1919 GAGAGAGCTCAGCCCAAGCCATCGAGACCT 1947
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Search completed: March 2, 2006, 03:32:03  
Job time : 1480 secs

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***This Page Blank (uspto)***

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Db 3590 GAATGTGAGAAACCTTCCACGAGCTCATCT.....CTTACTGTTATCAGAGA 3540
Qy 316 PheGluProProAsnAlaProLeuAsnArgLysGlyLeuValSerProGlnSerProGln 335
Db 3539 ATTCTACTGGAGAGAAACCATATGAGTGTAAGGACTGTGGAGGCGCTTCAACAGAG 3481
Qy 336 LysSerAspCysGlnProAsnSerProThrGluAlaCysSerSerLysAsnAlaCysIle 355
Db 3480 TCAACACCTTGTCC-----AGCACACAGATAACACACCGGAGAAAAAATATTGAAT 3428
Qy 356 LeuGlnAlaSerGlySerProProAlaLysSerProThrAspProLysAlaCysAsnTyr 375
Db 3427 GTAAGGAATGTAGGAAGCGCTTCAGCCAAATGTATCATC-----TTATTCAACATC 3377
Qy 376 LysLysTyrLysPheIleValLeuAsnSerLeuAsnGlnAsnAla-----LysProGly 393
Db 3376 AAGAATTC---ATCTGGAGAAACCATATTAATGTAAAGAGTGTAGAAAAGCCTTCA 3320
Qy 394 GlyPro-----GluGlnAlaGluLeuGlyArg-----LeuSer 404
Db 3319 GCCAGCGCTGCACACCTTGTCTCAGCATCAGAGAATTCATCTGGGAGAAAGCCTTATAAAT 3260
Qy 405 ProArgAlaTyrThrAlaProProAlaCysGlnProProMetGluProGluAsnLeuAsp 424
Db 3259 GTAAGGAATGTGGCAAGCGCTTCAGTGATGGCTCGCTCTTTGGCC-----GAC 3212
Qy 425 LeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIleProGlnAlaSer 444
Db 3211 ATCAGAGGTGTACA-----CTGGCAAAAGACCGTAGCAATGTATTGAATGTGGGA 3161
Qy 445 ArgLeuAsnAsnIleValAsnArg---SerMetThrGlySerProArgSerSerSerGlu 463
Db 3160 AAGCTTTTCAGCGAGAACACATCGCTTATCGTCACTGGAGATAT-TATCACACTGGGGAG 3102
Qy 464 SerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySerGlnSerPro 483
Db 3101 AAA-----CCCTTTGACTGCATCGACTGTGGCAAGCGCTTCAGC 3063
Qy 484 GlnHisAlaGluMetCysLeuHis----- 491
Db 3062 GATCATAGAGACTTATTTCAGCAGGAGATTTCATCTACTGAGAGAAACCTACAAATGT 3003
Qy 492 ---ThrAlaGlyProThrPheAlaGluMetGlyGluThrGlnSerGluTyrSerAsp 510
Db 3002 AATGTGTGTGGAAACCTTCAGC-----TACGGCTCATCCCTGACCGCTCCATCAGAGA 2949
Qy 511 SerSerCysGluAsnGlyAlaPhePheCysAsnGluCysAspCysArgPheSerGluGlu 530
Db 2948 ATTCACACAGGAGAGAAACCATATGAATGTGACATCTGTGGAAAGCCTTCAGCCATCAT 2889
Qy 531 AlaSerLeuLysArgHisThrLeuGlnThrHisSerAspLysProTyrLysCysAspArg 550
Db 2888 GCCTCACTACCCAGCAACCAAGAGTGCAATCTCGAGAGAGAGCCTTACCATTCAGAGGAA 2829
Qy 551 CysGlnAlaSerPheArgTyrLysGlyAsnLeuAlaSerHisLysThrValHisThrGly 570
Db 2828 TGTGAAAAGCTTTCAGCGAGAGCATACACCTTGCTAGCCATCTGAGGATCCCATCTGGA 2769
Qy 571 GluLysProTyrArgCysAsnIleCysGlyAlaGlnPheAsnArgProAlaAsnLeuLys 590
Db 2768 GAAAAACCCCTATGAATTAAGGAATGTGAAAAGCCTTTTAGCATCATCAGTTCACAGCTGGCT 2709
Qy 591 ThrHisThrArgIleHisSerGlyLysProTyrLysCysGluThrCysGlyAlaArg 610
Db 2708 ACTCATCAGAAATTCATCTGAGAGAAACCTTATGAATTAAGGAATGCGGAAAGCC 2649
Qy 611 PheValGlnValAlaHisLeuArgAlaHisValLeuIleHisThrGlyGluLysProTyr 630
Db 2648 TTCACACGAGGGCACATCTCGCACAGCACCACTAATAATTCATCTGGAGAGAAACCTTAC 2589
Qy 631 ProCysGluIleCysGlyThrArgPheArgHisLeuGlnThrLeuLysSerHisLeuArg 650
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Search completed: March 2, 2006, 04:05:09  
Job time : 630 secs

285 aProSerAlaArgAsnIaPro-----TyPheProCyAspIysAlaSerIy 301  
 374 CCMAATGTGATTTTACCCCAATCCTCAAGTATTTTGGTGGCCGCAATCA----- 428  
 301 sGIuGIuArgProSerSerGIuAspGIuIaIeAsuIaPheGIuProProAsnI 321  
 429 -----CATTCCTACCCCTGAAAATTG 448  
 321 aProLeuAsnArg-----LysGIuLeuValSe 330  
 449 CATGCCACACGCTGTTGTTTCAGAGCTGTAACTTTGAGCATGTAAGCTGTACTTCA 508  
 330 rProIInSerProGIuIysSerAspCyGIuInProAsnSerProThrGIuIaIaCySse 350  
 509 TCCGGAAGAGATGAGAGCGTTTGGAACTGCTCAGAGGAGACTCTATAGATGTGATGC 568  
 350 r-----LysAsnIaIaCyIleLeuGIuIaIaSerGIySerProProAlaIys----- 365  
 569 TGGAGAAATTACGGGAAATGTGTTCTCAGTCGTGCGT-AGACAGAGACTGAAAATATGATCA 627  
 366 -----SerProThraAspProIyAlaIaCyAsnIThrIyLysrTyIlys-----Ph 380  
 628 GAATTTTCTGAAGACACAAAGTACATGGGCTCTACTGGGAAAGATTCCAAAGATATT 687  
 688 TCTCGAGGTCTCAAGTTTAAAG-----AAGCTTATGAACGAGAGAGTCAGTCTGAAA 738  
 400 uGIyArgLeuSerProAlaIaTyThrAlaProProAlaIaCySGInProPrometGIuPr 420  
 739 AGGCGCGCTGGGGA-----ACTCC-CCT-----GG 761  
 420 oGIuAsnIeAspLeuGIuInSerProThrIyLeuSerAlaSerGIyGIuAspSerThrI 440  
 762 AGAAAGATGAACAGGAAATGCCAGATTTTGGTCAATGATGACAGTGAAGGAAAGCTAAC 821  
 440 eProGIuIaIaSerArgLeuAsn-----AsnIleValAsnArgSerMetThrGIySerPr 458  
 822 CCCCAGGGGAGAGAGAACGAGAAATATATGAATTTGGGAACAGCTTCACTGTGAATTC 881  
 458 cArgSerSerGIuSerHisSerProLeuIyMetHisProProIySeySthnSerCy 478  
 882 CAACCTTATTCACATCAGACAGACTCCCGTGGAGACAGACCCCAATAGTGTATGATG 941  
 478 sGIy-----SerGIuInSerProGIuHisIaIaGIuMetCySLeuHisIth 492  
 942 TAGCAAGAGCTTATTCAGAACTTCAGACTTATTCATACATCAGAGA-----ATCCAC 995  
 492 rIaIaGIyProThrPheAlaGIuGIuMetGIyGIuThrGIuInSerGIuTyrIserAspSerSe 512  
 996 TGGGGAAGAACCCCTAT-----GAATGTATATAGTGGGAAGCCCTTCACCCAGAGCTC 1049  
 512 r-----CySGIuAsnGIyAlaIaPhePheCyAsnGIuCy 523  
 1050 ACACCTTATTCAGATCAGAGATCCAGAAATCCACACTGAGAAAAAACCCTTATGATATGAGATTG 1109  
 523 sAspCyAsnArgPheSerGIuGIuAlaIaSerLeuIyAsnArgHisIthrIeuGIuInThrIaSerAs 543  
 1110 TGGGAAACCTTCACCTGAGCTGAGCTGCCTCACTTCGTGATCGAGAGATCCACACCGGGA 1169  
 543 pIyAspProIyIySeyAspArgCySGIuAlaIaSerPheArgTyIySGIuAsnLeuAlaSe 563  
 1170 GAACACCTTATGATATGATGAGTGTGGGAAGACTTCACAGCTGAGACTCACACCTCACCA 1229  
 563 rHisIyThrValHisIthnGIyGIuIyAspProTyArgCyAsnIleCySGIyAlaGIuPh 583  
 1230 CCATCAGAGAAATCCACACTGATGAAGAAACCTTACCCCTGCATGATATGGGAAGCCCTT 1289  
 583 sAsnIleProAlaAsnLeuIyThrHisIthnArgIleHisSerGIyGIuIyAspProTyIy 603  
 1290 CAGCAGAGACTCAACCTTATTCACATCAGAAATCCACACTGGAGAAAAAACCCTTATGA 1349

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QY      603  bCySgUthtCySgUlylaahrgPheValGlnValaIahIstleuAryglaIahIstValleuI 623
Db      1350  ATGTAAATGAAATGTGGGAAAGCCCTTCAGCCAGCTACACCTCATATAGACACAGAAAT 1409
QY      623  eHtstHlyGlyluAaProTyProCySgUlleCySgUlyThArGrPheArghIstleuG 643
Db      1410  CCACACTGTGAGAGAAAGCCCAACGAATGTATGGAATGTGGAGAAAGTTTACTCTACAGTTTC 1469
QY      643  nThleuIysSerHtstleuArygIleHtstHngUlyGlyluAaProTyHtstCySgUlyuY 663
Db      1470  AGGCTTATTCAGCATCAAGAAATCCACACCGGGAGAACCCCTATGAATGTAGTCAAGT 1529
QY      663  sArstleuHtstPheArghIstIysSerGlnleu-----ArgleuHtstleuAryG 679
Db      1530  TGGAGAAAGCTTCAGGTACAGTACGCTCTGTGTTGCCATCAGAGAAATTCACACTGGAGA 1589
QY      679  nLyAhIs---GlyAlaIleThraHtstHtIysValGlnTyArGyAlSerAlthraPle 698
Db      1590  GAACCTTGAATGGGATCGGCAGTACGACAAAGCTCCTCATAGTTACG---ACCGAGTT 1646
QY      698  u 698
Db      1647  A 1647

RESULT 15
US-10-185-44166/c
; Sequence 44166, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PATTON, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44166
; LENGTH: 4305
; TYPE: DNA
; ORGANISM: Bovine 19866880546157
US-10-750-185-44166

Alignment Scores:
Pred. No.: 8.46e-21 Length: 4305
Score: 462.00 Matches: 147
Percent Similarity: 42.0% Conservative: 59
Best Local Similarity: 30.0% Mismatches: 214
Query Match: 12.2% Indels: 73
Gaps: 18

US-10-755-8889-18 (1-706) x US-10-750-185-44166 (1-4305)

QY      242  TySerArGrProthleuGlnuValSerProAenValCyHtstSerAenIleTyr---Sex 260
Db      3740  TATAACAACCTGAGAAATTTGTTCTCTACACAGATTTGGAGAGAAATATTATGATTAAT 3681
QY      261  ProLySgUthHtIleProGlnGlnuAlaIrgSerAepMet-----HtstYSerVal 277
Db      3680  CACAAGTCAGATGAAAAAAACTTTTCCAGAAATTCATGTAATTAAAAACAGAAAGTA 3621
QY      278  AlagUglyLeuLyProAlaAlaProSerAlaIrgAenAlaProTyRPhProCyAep 297
Db      3620  TATGAGAGAAAGAAA-----CTTTTAATATGTAAT 3591
QY      298  LyAlaSerLySgUglyGlnuArGrProSerSerGlnuAepGlyIleAlaIleuHtst----- 315

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Db      984 GAATCAACAGAAAAAGCTGTGAAAAACAG-----ATGAGAGAGACAAAGACAG 1034
Qy      381 eValLeuAaSerLeuAaInLeuAaLeuAaProGlyGlyProGluGlnAgluLeuG1 401
Db      1035 CATCAGGAGAGCAATCAGCAAGCAAGAGTACGCAATATTAAGACAGACAGAGAG 1094
Qy      401 YATgLeuSerProAglAaTyrThraAProProAaCyGlnProMeGluProG1 421
Db      1095 TGAGGACATCGAGAGAGAGCTTG-----CATCGAGCCACACA 1130
Qy      421 uAaLeuAaPLeuGlnSerProThryLeuSerAaSerGlyGluAaPserThr1lePr 441
Db      1131 GCATATACACACACAGACT--ATGCTATAGACAGAGAGCAGTAG----- 1176
Qy      441 oGlnAaSerAaArgLeuAaAaInLeuAaAaSerMetThrcylserProAaGserse 461
Db      1177 -CAAGGCAACGATGTGAGAAACATT-----AATGAAACCTCTTACCTTACTTACA 1226
Qy      461 rSerGlnSerHisSerProLeuTyrMetHisProProLysCyThrSerCyGly----- 479
Db      1227 GCAGAAAAACCAATGCTGTAAAGAAATTACAT-----AAATGTGATGAATGTGGGAATC 1280
Qy      480 -----SerGlnSerProGlnHisAaGluMetCysLeuHisThr----- 492
Db      1281 CTTCAATATATATATCCGCTGTTCACATAAATTATG-----CACACTGGGGAATA 1334
Qy      493 -----AaGlyProThrPhe----- 497
Db      1335 GCGCTATGATGTGATGACTGTGAGAGGACTTCCGGAGCAGCTCGAGCTTCGGGTCCA 1394
Qy      498 -----AaGluGluMetGlyGluThrGlnse 506
Db      1395 CAACCGATCCACACTGGGAGGAAAGCCGTACAACTGTGAGAAATGTGGAAAGCCTCAT 1454
Qy      506 rGluTyrSer-----AaPserSerCyGluAa 515
Db      1455 GTCTCTACTCCAGCCTTATTAACCAAAAGACACCATTCTGGGAGAAAGAACTGTAAA-- 1512
Qy      515 nGlyAaPhePheCyAaInGluCyAaPcyAaArgPheSerGluGlnAaSerLeuAaPAr 535
Db      1513 -----TGTGATGATGATGTGAAAAATCCCTTCAATTATGACTGTCTGTGAGCA 1559
Qy      535 gHiThrLeuGlnThrHisSerAaPLeuProTyrLeuCyAaPArgCyGlnAaSerPh 555
Db      1560 GCATTAAGATCCACACTGGGAGAGAACCTTAAGATGTGTGAGTGTGGAAAGCCTT 1619
Qy      555 eArgTyrLeuGlyAaInLeuAaSerHisLeuThraHisThrcylGluTyrProTyrAr 575
Db      1620 CAGGAACAGCTCTGGGCTCAGAGTCCACAAAGAGTCCACAGGGGAGAGAGCCCTATGA 1679
Qy      575 gCyAaInLeuCyGlyAaGlnPheAaAaArgProAaAaInLeuAaSerThrHisThraG1 595
Db      1680 ATGGACACATCTGTGGGAAACCTTCACTAACAGCTCTGCTTGGGCTTCAATAAAGAT 1739
Qy      595 eHisSerGlyGluAaPLeuProTyrLeuCyGlnThrcylGlyAaArgPheAaGlnValA1 615
Db      1740 CCACACAGGTAGAAACCTTACGAATGTGATGAGTGGAGAAAGCCCTTACTTACTTGAAG 1799
Qy      615 aHisLeuAaGlnHisValLeuLeuHisThrcylGluTyrProTyrCyGlnLeuCy 635
Db      1800 AACACTTCTCAACCAATAAAGATCCATTGGAGATTAACCTTAATGAATGATGAGAGTG 1859
Qy      635 eGlyThraArgPheArgHisLeuGlnThrLeuAaSerHisLeuAaG1leHisThrcylG1 655
Db      1860 TGAGAAATCTTTATATAGCTCTTCTCATTCAGATTAAGTCAATCCACACGTGAGAG 1919
Qy      655 uLysProTyrHisCyGlnTyrCyAaInLeuHisAaPheArgHisLysSerGlnLeuAaArg 675
Db      1920 GAAACCCATATGTGTGATGAGTGTGGAGAGGCTTCAGAAACAGCTCAGGCTCACAAGT 1979
Qy      675 uHisLeuAaArg 678
Db      1980 GCATTAAGG 1989

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RESULT 14
US-11-072-512-816
; Sequence 816, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISOMO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KENICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 816
; LENGTH: 2634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-816

Alignment Scores:
Pred. No.: 4,9e-21 Length: 2634
Score: 462.50 Matches: 162
Percent Similarity: 39.9% Conservative: 70
Best Local Similarity: 27.9% Mismatches: 258
Query Match: 12.2% Indels: 93
DB: Gaps: 21

US-10-755-889-18 (1-706) x US-11-072-512-816 (1-2634)

Qy      172 AlaProGlyCyGlnSerAaGlnAaPheAaPProSerLeuTyrSerGlyLeuSerThrPro 191
Db      20 TCCCGGATGTGTGGTGTGTGACAGGGTCCAAAGGCGCTGTGTC--GTGTCCGATCC 76
Qy      192 ProAaSerTyrSerMet-TyrSerHisLeuProAaAaSerSerLeuAaPheSerAaPgl 211
Db      77 CCAATATCTGTGCTCTCCGCCCCCAGGCTCTTCCATAAAGTCTGCTTCCGACAA 136
Qy      211 uGlnPheArgAaPValArgMetProValAaAaPProPheProLeuGlyAaGlnAaLeuPr 231
Db      137 GAGACGCTGGGAGATGAGATGTGCGGCTGCGCTCTTAAGGCCAAAGTCCAGGTGAG 196
Qy      231 oCyAaPserAaArgProValAProGlyGluTyr-----SerAaGProThrLeuG1 248
Db      197 CTGGGTCCGCTTATCTTTTCCATTTCTGTGCAATGACATCCATCCATCCAGAGC 256
Qy      248 uValSerProAaVal-----CyHisSerAaInLeuTyrSerProLysGluThr11 265
Db      257 TTTAACCTTATCTCTCCATCAGGCCCAAGTGTCTGCTGCGTGAATGAGAGCCTC 316
Qy      265 eProGluGlnAaArgSerAaPMetHisTyrSerValAaGluGlyLeuAaPProAaA1 285
Db      317 ACCTTATCTTGGACCTCTGTCTCTTCCACCCCTGTCTCCCTT---CTTCCCTT 373

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Qy 339 CysGlnProAsn-----SerProThrglnAla 347
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Db 412 AGAGGCGCCGAGGCTCTGAAGTTCGTGACGTGCGCCGTGACTTCTCCCGAGAGAGTGG 471
Qy 348 CysSerSerlysaAsnAlaCysIleLeuGlnAlaSerGlySerProProAlaLysSerPro 367
   |||
Db 472 -----GGCTGCTCGCGGCCCGCCGACAGAGGCC----- 498
Qy 368 ThrAspProlysaAlaCysAsnTrpLysLysLysPheIleValLeuAsnSerLeuAsn 387
   |||
Db 499 -----CTGTACCGGAGCGGTGATGCGGAGACCTACCGT 531
Qy 388 GlnAsnAlaLysProGly-----GlyProGlnGlnAlaGluLeuGlyArgLeuSerPro 405
   |||
Db 532 CACCTGGGCGCGCTCGGTCGCGAGGTCCCAACACGACCTCTCTCTGTTGGAAACA 591
Qy 406 ArgAlaLysThrAlaProProAlaCysGlnProProMetGlu---ProGlnAsnLeuAsp 424
   |||
Db 592 AACACCGATGACTGGAAACCGGCTGCTGATCCGAGAGTACCGAGAGGCTTACA 651
Qy 425 LeuGlnSerProThryLysLeu---SerAlaSerGlyLysAspSerThryLysPro----- 441
   |||
Db 652 GTCCAGAGAAAGAACACAGAACAGAAAGATGGGAGAGAAAGATATTCGCGCTAAG 711
Qy 442 GlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThryLysSer-----ProArg 459
   |||
Db 712 GAGGCAACCCGAAAGGAGGAGGAGGCGGAGGCCGACAAACCCGACGATTCCTAGG 771
Qy 460 SerSerSerGlnSerHisSerProLeuLysThryMetHisProProLysCysThrySerCysGly 479
   |||
Db 772 CAGACGTCGCGGGCC-----CCCATCTGCTCCGATCGCGGC 807
Qy 480 SerGlnSerProGlnHisAlaGluMetCysLeuHisSerThryAlaGly----- 494
   |||
Db 808 TGTACTTCTCTGATCATCAGGCGCTGAGAGCCAGCAAGTGGCGCCGAGAACTTAAAAAG 867
Qy 495 -----ProThrPheAlaGluGluMetGlyLysLysLysGlnSerGlyLysSerAsp 510
   |||
Db 868 CTTTACCTTGGCCGACGTGAGCGCGCTTCTTCTATCCATCCCTGCTGTGATGATCAG 927
Qy 511 SerSerCysGlnAsnGly-----AlaPhePheCysAsnGlyCysAspCysArgPheSer 528
   |||
Db 928 CGGGGGGACACACTCGGAGAGTGGCCCTATGTTGTGACAGTGTGGAAACGTTTCTCC 987
Qy 529 GlnGlnAlaSerLeuLysArgHisThrLeuGlnThryHisSerAspLysProThryLysCys 548
   |||
Db 988 CAGCGCAAGAACCTCTCCACAGCAGGTATCCATACAGGGGAGAAAGCCCTATCAGTGC 1047
Qy 549 AspArgCysGlnAlaSerPheArgTrpLysGlyAsnLeuAlaSerHisLysThrValHis 568
   |||
Db 1048 CTTGACTGTGGTCTGCTCTCCGAGAGCGGCTCTTGGCCATACCGGACACACACAC 1107
Qy 569 ThrGlnGlyLysProThryArgCysAsnIleCysGlyAlaGlnPheAsnArgProAlaAsn 588
   |||
Db 1108 ACAAGTGAATAAACCCACACAGTGCCTTAGCTGTGAAGTGGCTTCCCTACCCCTCCG 1167
Qy 589 LeuLysThryHisSerArgHisSerGlyLysProThryLysCysGlnThryCysGly 608
   |||
Db 1168 CTAGCATTCACACAGCTACACACACAGGAGAAAGCCCTACACTGCTCGAGTGGCAAC 1227
Qy 609 AlaArgPheValGlnValAlaHisLysLeuArgAlaHisValLeuIleHisThrGlyGlyLys 628
   |||
Db 1228 CGCGGCTTCCGACAGCGACGCGCTCTGATCCACACGCGCATCCACACAGGAGAGAG 1287
Qy 629 ProThryProCysGlnIleCysGlyThryArgPheArgHisLysGlnThryLysSerHis 648
   |||
Db 1288 CCTTACCCGCTGCGGAGCTGAGAGGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1347
Qy 649 LeuArgIleHisThrGlyLysLysProThryHisCysGlyLysCysAsnLeuHisPheArg 668
   |||
Db 1348 CGGGGTGTGCACTCTGGGAGAGGTCTCTATGCTGCGAGCACTGTGAGAGCGCGCTTCTCC 1407
Qy 669 HisLysSerGlnLeuArgLeuHis 676

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Db 1408 CAGCGCAGCAGCGCTGCTCCAGCAC 1431
RESULT 12
US-11-072-512-693
/ Sequence 693, Application US/11072512
/ Publication No. US2006002945A1
/ GENERAL INFORMATION:
/ APPLICANT: ISOGAI, TAKAO
/ APPLICANT: SUGIYAMA, TOMOYASU
/ APPLICANT: OTSUKI, TETSUJI
/ APPLICANT: WAKAMATSU, AI
/ APPLICANT: SATO, HIROYUKI
/ APPLICANT: ISHII, SHIZUKO
/ APPLICANT: YAMAMOTO, JUN-ICHI
/ APPLICANT: ISONO, YUUKO
/ APPLICANT: HIO, YUKI
/ APPLICANT: OTSUKA, KAORU
/ APPLICANT: NAGAI, KEIICHI
/ APPLICANT: IRIE, RYOTARO
/ APPLICANT: TAMECHIKI, ICHIRO
/ APPLICANT: SEKI, NAOTIKO
/ APPLICANT: YOSHIKAWA, TSUTOMU
/ APPLICANT: OTSUKA, MOTYUKI
/ APPLICANT: NAGAHARI, KENJI
/ APPLICANT: MASUHO, YASUHIKO
/ TITLE OF INVENTION: Novel full length cDNA
/ FILE REFERENCE: 084335-0191
/ CURRENT APPLICATION NUMBER: US/11/072,512
/ CURRENT FILING DATE: 2005-03-07
/ PRIOR APPLICATION NUMBER: US 60/350,978
/ PRIOR FILING DATE: 2002-01-25
/ PRIOR APPLICATION NUMBER: JP 2001-379298
/ PRIOR FILING DATE: 2001-11-05
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 693
/ LENGTH: 2241
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-072-512-693
Alignment Scores:
Pred. No.: 3,6e-21 Length: 2241
Score: 463.50 Matches: 122
Percent Similarity: 42.7% Conservative: 47
Best Local Similarity: 30.8% Mismatches: 139
Query Match: 12.2% Indels: 88
DB: 9 Gaps: 14
US-10-755-889-18 (1-706) x US-11-072-512-693 (1-2241)
Qy 347 AlaCysSerSerlysaAsnAlaCysIleLeuGlnAlaSerGlySerProProAlaLysSer 366
   |||
Db 864 TCCTGTAGTGGCATCTCTCTCTGATCATCAAGGAGCTGATCTCT-----TTACCC 917
Qy 367 ProThrAspProlysaAlaCysAsnTrpLysLysLysPheIleValLeuAsnSerLeu 386
   |||
Db 918 CCACCATTAACA-----TCTTCC-----ATATCTTCTCTGTAGACAGACTTTA 962
Qy 387 AsnGlnAsnAlaLysPro-----GlyGlyProGlnGlnAlaGluLeuGlyArg 402
   |||
Db 963 CACTCTTAAGCTTCAAGTATCTCTTATTTGAAACAAGGAGAAAGCGCTGGATGGT--- 1019
Qy 403 LeuSerProAlaGlyLysThryAlaProProAlaCysGlnProProMetGluProGlnAsn 422
   |||
Db 1020 ---TGGCAGAGAGCTTAC-----AAGAGGCTGTGCTTCAGATCTGGA 1058
Qy 423 LeuAspLeuGlnSerPro-----ThryLysLeuSer 432
   |||
Db 1059 ATCATGTGTAAACCAAGATTATTTCTTAAGAGAAAGACTTTATGAAATGAAATTATG 1118
Qy 433 AlaSerGlyLysAspSerThryLys-----Pro-GlnAlaSerArgLeuAsnAsnIle 449

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Db      1102 AATGTAATATGCGCAAGCTCT-----CAATGAATGCA 1140
Qy      340 1nProanserProthrgluAaCyseSerlysaAnaCyrlleuGlInlaSerg 360
Db      1141 CACCT-----TACGACATCA 1158
Qy      360 lYserPro-ProAlaIySerProthrapProlyAaCybaAntrlys---lystrY 378
Db      1159 AGATTCATCTCGAAGAAACCTTATGATGTAAGAAATGGCAAGCTCTTCAGGCAC 1218
Qy      379 lYsPheIleValleuAn-----SerleuAn 387
Db      1219 AAGTTTGTCTACCAATCATCTAGAAATGACACGGAGACCACTTACAAATGTAAT 1278
Qy      388 GlAnaAlaIyPro-GlyGly----- 394
Db      1279 GAATTTGGAGGCGCGAGGCGGTGATCATGAGTCAGAGATCGAGACCATCTGCTTA 1338
Qy      395 -----ProGlulAlaGlulEuGlYagLeuSerProArghAlaYrThrl 410
Db      1339 ACAAGGTGAACCCCTCTCTACTTAAATAATTAACAAATTAAGCCGGCGCGGCGGC 1398
Qy      410 aPro-----ProAlaCyseGlInProProMetGlUProGluaAnleuAspleuGlInserP 428
Db      1399 GCGTGTAGTCCAGCTACTCG-----GAGGCTGAGGCGAGAAATGGCTGAAC 1449
Qy      428 oThrlYleuSerAlaSer-----Gl 435
Db      1450 CGGGAAGCGGAGCTTCAGTAGACCGAGATGGCCACCTGACGTCCGAGTCCGCGCTG 1509
Qy      435 YgluAspSerThrllePro-----GlAlaSerArgleuAs 447
Db      1510 GCGACAGAGGAGACTCCGTCTCAAAAAAACAACAACAACAACAACAACAACAACA 1569
Qy      447 naenIleValAsnArgSerMetThrglySerProArgSerSerSerGluserHisSerP 467
Db      1570 AATGTAAATGATGTGGCAAGTCTTC-ACTTACATTCACACCTTGACACAAATCAGAG 1628
Qy      467 oleuTYMet-----HisProProlyCyseThrSerCyseGly-----SerInse 482
Db      1629 AATACATCTCGAGAGAACTTACAAATGACAGTGTGGCAAGATTTATGTGACT 1688
Qy      482 rProGlInHlaGlumecYleu-----HisThrlaGlYProth 496
Db      1689 TCCG-----TGCTTACACGACATCAAGATTTCACACT----- 1722
Qy      496 rPheAlaGlulMetGlyglInThrgInserGluTYrSerAspSerSerCyseGluAnGl 516
Db      1723 -----GAGAGAGA----- 1731
Qy      516 yAlaPhePheCyAsnGlucYsaAspCyAsArgPheSerGlulAlaSerleuYsaArgH 536
Db      1732 -CCTTACAATGTATGATGTGGCAAGATTTAGAGACTGTTCAGGCTTACGCGCA 1790
Qy      536 eThrlEuGlInThHiserAspIyProTYrlyCyAsArgCyseGlInlaSerPheAr 556
Db      1791 TCTATCAATTCACATCGAGAAACCTTACAAATGTAAGAAATGTGCCAAGCTCTTCAG 1850
Qy      556 gTYrlyGlyAsnleuAlaSerHislystrYValHisThrglyGluYrProTYrArgY 576
Db      1851 GCATAGTTTATCCCTTAAGCATCTCAGAGATTTCATACCGAGAGAAACCTTACAGATG 1910
Qy      576 saenIleCyseGlyAlaGlInPheAsnProAlaAsnleuYstrHisThrglyIleH 596
Db      1911 TGAATGATGTGGAGGACTTCACTGAAATTCAAACCTTGCAATCATCAGAAATCCA 1970
Qy      596 eSerGlyGluYrProTYrlyCyseGluThrgYseGlyAlaArgPheValInAlaIleH 616
Db      1971 TACTGAGAGAAACCTTACAAATGCAAGTGAATGCAAAAGCTTTATGTACAAATTCACA 2030
Qy      616 sIeuArgAlaHleValleuIleHisThrglyGluYrProTYrProCyseGluIleCyseG 636
Db      2031 CTTTGCAGACATGAGCAATTCATCTGAGAGAGAGTCTTACAAATGCAATGATGTG 2090

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Qy      636 YThrgPheArgHleleuGlInThrlEuYSerHisleuArgIleHisThrglyGluY 656
Db      2091 CAAGGTCTTCAGCCCAAGTTATACCTTAATAAAGATGAGAAATTCATCTGGGAGAA 2150
Qy      656 sProTYrHisCyseGluYrCyAsnleuHisPheArgHleYstrGluY----- 673
Db      2151 ACCGTACAGATCTCATGATGTGTAGAGACTTCACTGAAATTCAAACCTGCAATCA 2210
Qy      674 ----ArgleuHisleuArgGluYs 680
Db      2211 TCAGAAATTCATCTCGAGAGAAA 2235

RESULT 11
US-10-517-151-3
/ Sequence 3, Application US/10517151
/ Publication No. US20060019252A1
/ GENERAL INFORMATION:
/ APPLICANT: Nakamura, Yusuke
/ APPLICANT: Furukawa, Yoichi
/ APPLICANT: Oncotherapy Science, Inc.
/ APPLICANT: The University of Tokyo
/ TITLE OF INVENTION: Genes and Polypeptides Relating to Hepatocellular or
/ TITLE OF INVENTION: Colorectal Carcinoma
/ FILE REFERENCE: 082379-000400US
/ CURRENT APPLICATION NUMBER: US/10/517,151
/ CURRENT FILING DATE: 2004-12-06
/ PRIOR APPLICATION NUMBER: US 60/386,985
/ PRIOR FILING DATE: 2002-06-06
/ PRIOR APPLICATION NUMBER: WO PCT/JP03/07070
/ PRIOR FILING DATE: 2003-06-04
/ NUMBER OF SEQ ID NOS: 111
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 2744
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (343)..(1845)
/ OTHER INFORMATION:
US-10-517-151-3

Alignment Scores:
Pred. No.: 4,06e-21 Length: 2744
Score: 464.00 Matches: 135
Percent Similarity: 39.5% Conservative: 50
Best Local Similarity: 28.8% Mismatches: 205
Query Match: 12.2% Indels: 78
DB: Gaps: 14

US-10-755-889-18 (1-706) x US-10-517-151-3 (1-2744)
Qy      259 TYrSerProlyeGlulThrlle-----ProGlulAlaArgSerAspMetHis 274
Db      112 TTTTCCCAAGGACATCTTCGCGCTTTCACCCAAAGTTCGGGACGAGATTTCGTAAT 171
Qy      275 TYrSerValAlaGlulYleuYsProAlaAlaProSer-----AlaArg 289
Db      172 AACAGAAAGATTTCCGTTAGCCCGGCGGAGCAAAATTCGATTCCTCGGCGCTCC 231
Qy      290 AsnAlaProTYrPheProCYsaAspIyAserlyGluGlulArgProSerSerGlu 309
Db      232 CCGGCGCACCTGAGCCCTGTGTCGCGAGGAGCTCTCGATCCAGAGGCTCCAGGCGCC 291
Qy      310 AspGlulAlaLeuHisPheGlu-----Pro 318
Db      292 GAGGCGCGAGGCTTGACACGGAAGGCCGTGGCGCGCTTCGCGGTCCATGCGGCCA 351
Qy      319 ProAnaIaProleuAnaArglyGlyleuValSerProGlInserProGlInlySerAsp 338
Db      352 CTTTGGCTCCGCTCCCTGCGAGGAGCAGAAAGGCCAGACCCAGTGGAAAGAGGCGC 411

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; LENGTH: 3078
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-622

Alignment Scores:
Pred. No.:      3,896-21      Length:      3078
Score:          465.00      Matches:      98
Percent Similarity: 49.8%      Conservative: 31
Best Local Similarity: 37.8%      Mismatches: 106
Query Match:      12.3%      Indels:      24
DB:               9          Gaps:      4

US-10-755-889-18 (1-706) x US-11-072-512-622 (1-3078)

QY 472 ProProlyscYsrhSerSerGlySerGlnSerProGlnHsAlaGluMet----- 488
DB 799 CCTTACAAATGTGAAGATGTGGCAAGCTTTTAAACCGTCTCAAACTTACTTAAACAT 858
QY 489 ----CysLeuHsIsthAla----GlyProThrPheAlaGluGluMetGlyGlu----- 503
DB 859 AAAATAATCTACTCTGAGAGAAACCTTACAAATGTGAAGATGTGGCAAGCTTTTAAAC 918
QY 504 -----ThrgInSerGluTrSerAspSerSerCysGluAengIyAlaPhePheCys 520
DB 919 CGGTCTCAACCTTACTTAAACATTAAGATTATCATACAGAGAGAAACCTTACAAATGT 978
QY 521 AsnGluCysAspCysArgPheSerGluGluAlaSerLeuIyAsrGhIsthLeuGlnThr 540
DB 979 GAAGAAATGTGGCAAGCTTTTAAACAGTTCTCGATTCTAATAACATTAAGAGAAATTCAT 1038
QY 541 HsSerAspIyProIyTrIyCysAspArgCysGlnAlaSerPheArgTrIyGlyAsn 560
DB 1039 ATGGAAGATTAACCTTACAAATGTGAAGATGTGGCAAGCTTTTAAAGTATCTCAATT 1098
QY 561 LeuAlaSerHsIyIsthValHsIsthGlyGluIyProIyArgCysAsnIleCysGly 580
DB 1099 CTTAAAAACATTAAGATATCATCTAGTGGAGAAACCATTAATGTGAAGATGTGGC 1158
QY 581 AlaGlnPheAsnArgProAlaAsnLeuIyIsthIsthArgIleHsSerGlyGluIy 600
DB 1159 AAAGCTTTAACAGTCTTCAAACTTACTTAAACATTAAGATATTCATACATGAGAGAAA 1218
QY 601 ProIyTrIyCysGluTrIyCysGlyAlaArgPheValGlnValAlaHsLeuArgAlaHs 620
DB 1219 CCTTACAAATGTGAATGTGGCAAGCTTTTAAACAGTCTTCAACCTTACTTAAACAT 1278
QY 621 ValLeuIleHsIsthGlyGluIyProIyProCysGluIleCysGlyThrArgPheArg 640
DB 1279 AAAAGAAATTCATACGGAGAGAAACCTTACAAATGTGAAGATGTGGCAAGCTTTTAAA 1338
QY 641 HsIsthGlnThrLeuIySerHsIsthLeuArgIleHsIsthGlyGluIyProIyTrIyCys 660
DB 1339 CAGTCTCAACCTTACTTAAACATTAAGATATTCATCTAGGAGAGAAACCTTACAAATGT 1398
QY 661 GluIyCysAsnLeuHsIsthPheArgHsIsthSerGlnLeuIyGluHsIsthLeuArgGln--- 679
DB 1399 GAAAAATGTGGCAAGCTTTTAAAGTGTCTCAGCTTTTAAACATTAAGAGAAATCAT 1458
QY 680 -----LysHsGlyAlaIleHsIsthArg 687
DB 1459 ATGGAAGATTAACCTTACAAATGTGAAGATGTGGCAAGCTTTTAAAGTATTCATCAAC 1518
QY 688 LysValGlnTrArgValSerAlaThrAspLeuProGluLeuProIyAsnIleCys 706
DB 1519 CTTACTTAAACATTAATATTCATCTAGAGAGAAACCTTACAAATGTGAAGAAATGT 1575

RESULT 10
US-11-072-512-1127
; Sequence 1127, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO

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; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKUJI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1127
; LENGTH: 2724
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-1127

Alignment Scores:
Pred. No.:      4,036-21      Length:      2724
Score:          464.00      Matches:      158
Percent Similarity: 38.5%      Conservative: 62
Best Local Similarity: 27.7%      Mismatches: 167
Query Match:      12.2%      Indels:      187
DB:               9          Gaps:      21

US-10-755-889-18 (1-706) x US-11-072-512-1127 (1-2724)

QY 231 ProCysAspSerAlaArgProValProGlyGluTrSerArgProThrLeuGluValSer 250
DB 723 CTTGTTCACACATTAAG-----AATTCATACGAGAGAGAAAGCTTACAAAGTGTCA 773
QY 251 ProAsnValCysHsIsth-----AsnIleTrSerProIySerGluThrIleProGluGluAlaArg 270
DB 774 TG-AATGTGGCAAGCTTCAATGCAATTCACCTTGCACGACATCAGAGAAATACATA 832
QY 257 -----AsnIleTrSerProIySerGluThrIleProGluGluAlaArg 270
DB 833 CTGAGAGAGAAACCTTACAAATGTGATGATGTGT-GGCAAGCTTCACTCAAAATTCAC 891
QY 271 SerAspMetHsIyTrSerValAlaGluGlyLeuIyProAlaIleProSerAlaArgAsn 290
DB 892 CTTGCAATTCATCACAGAAATCACACATCGAGAGAAACCT----- 930
QY 291 AlaProIyTrPheProCysAspIyAlaSerIy----- 301
DB 931 -----TACAATGTAATGAGGTGTGGCAAGCTTCAACAAAAATGCACACCTTGCA 981
QY 302 -----GluGluGluArgPro-SerSerGluAspGluIleAlaLeuHsI 315
DB 982 CGACATCAGAAATTCATAGTGTGAGAGAGAAACCTTAAAGATGTGAAGATGTGGCAAGCA 1041
QY 315 sPheGluProProAsnAlaProLeu----- 323
DB 1042 TTTTCAGGGGTTTCAGGCTTACGTCTCATCTTGAATTCACATCGAGAGAAACTTAC 1101
QY 324 -----Asn-ArgIyGlyLeuValSerProGlnSerProGlnIySerAspCysG 340

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QY	203	ValSerSerLeuLeuPheSerAspGluGluPheArg-----AspValAla-----	217
Db	999	GTGATGTAATGTGGCAAGATCTTCAGAAAAAATTCATATTTTGTGAAGACCAAGAGAGCTC	1058
QY	218	-----MetProValAlaAsnProPheProlyGluArg	228
Db	1059	ACACTGGACAGAAACCTACATATGTATGTAATGTGGCAAGCTCTTATGTAAGTAAGTTCC	1118
QY	229	AlaLeuProCybAbspSerAlaArgProValProGlyGlyTyrSerArg-----Pro	245
Db	1119	ACCTTG-----CAGTTCATCAGGAATTCATACCG	1148
QY	246	ThrLeuGluValSerProAsnValCysHisSerAsnLeuTyrSerProlyGluThrIle	265
Db	1149	GTGAAAAACCTTACAAATGTAATCTGTGTGGGAATCC-TTTAGT-----	1192
QY	266	ProGluGluAlaArgSerAaspMetHisTyrSerValAlaGluGlyLeuLysProAlaAla	285
Db	1193	---CAGCGTGTCCATCTTAAGCTTACAGACGTTCACTACGAGAGAGACC-----	1243
QY	286	ProSerAlaArgAsnAlaProTyrPheProCybAplySalAserLyGluGluArg	305
Db	1244	-----TTCAAAATGTAATGATGTGTGGCAAAACCTTTAAACGG	1279
QY	306	ProSerSerGluAbspGluIleAlaLeuHis-----PheGluProPro-----	319
Db	1280	AGCTCAAC-----CTCATGTATACATCAGTAATTCATCGACGAAAGAAACATAT	1330
QY	320	-----AsnAlaProLeuAsnArgLysGlyLeuVal--SerProGlns	333
Db	1331	AAATGTATGTAATGTGGCAAGCATTCAGACATTAATCTTGTATGTACCCGAGA	1390
QY	333	erProGluLysSerAaspCysGlnProAsnSerProThrGluAlaCysSerSerLySaAsn	353
Db	1391	ATCCACAGTGGAGAGAAGAAC-AATACAAATGCATGAATGTGGCAAGCTCTTCAGTAAGCG	1449
QY	353	IaCysIleLeuGln-----AlaSerGlySerP	362
Db	1450	TTCAAGTCTTGGACGATCGACGAATTCACACTGTAGAGAAACCTTCAAAATGCATGA	1509
QY	362	roProAlaLysSerProThrAaspPro-LysAlaCysAsnTplyLysTyrIlyPheIle	381
Db	1510	ATGTGGCAAGGCTTCAGTAAACGTTCAAGCTTCAGT-----	1548
QY	382	ValLeuAsnSerLeuAsnGlnAsnAlaLysProGlyGlyProGluGlnAlaGluLeuGly	401
Db	1548	-----	1548
QY	402	ArgLeuSerProArgAlaTyrThrAlaProProAlaCybGlnProMetGluProGlu	421
Db	1549	---GCATCAGAAATTCATACTGACA-----GAA	1575
QY	422	AsnLeuAapLeuGln-----SerProThrLyLeuSerAla	433
Db	1576	AACTTACAAATCAATAAATGTGGCAAGGTGACAGTAAGCATTCACATCTTCGACGTGA	1633
QY	434	SerGlyGluAaspSerThrIleProGluAlaSerArgLeuAsnAsnIleValAsnArgSer	453
Db	1636	TT-GGAGAA-----TTCATACCG---GGGAGAAAGCTTATTAATGACATGAATGT-GGC	1684
QY	454	MetThrGlySerProArgSerSerSerGluSerHisSerProLeuTyrMet-----His	471
Db	1685	AAAGTTTTCAGATCAATTCACAGACTTCGACCTTCACAGAAATTCATCTCGAGAGAAA	1744
QY	472	ProProLybCysThrSerCybGlySerGlnSerProGlnHisAlaGluMetCysLeuHis	491
Db	1745	CCCTTACAAATGCAATGAATGTGGCAAGGCTTCAGTCAACATTCACAGCTTTCAGTGCAT	1804
QY	492	Thr-----AlaGlyProThrPheAlaGluGluMetGlyGluThrGlnSer	506
Db	1805	CGGAGAAATTCATACGTGAGAGAAACCTTACAAATGCAAGAAATGTGGCAAGGTC-----	1855
QY	507	GluTyrSerAaspSerSerCys-----GluAsnGlyAla	517

Db	1859	---	TTCAAGTACCGCTTTCAGCTTTTTCGAAAGCATCGAAGAAATTCATCTACGAGAGAAACCT	1915
Qy	518	Phe	heCyaaenGluCyaaepCyaaArgPheSerGluIuIaSerLeuLyaaArgHisThr	537
Db	1916	TACAAAGTACAAAGAAATGGCAAGCTTCTCAAGTCAAAAGTTCAACCTTTACAGTGCATCGG	1975	
Qy	538	Leu	GlnThrHisSerAspLeuProTyrLeuCyaaAspArgCyaaGlnIaSerPheArgTyr	557
Db	1976	AGAATTCACTAGTGGAGAGAAACCTTACAAATGCATGAATCGCGCAAGGTCTACAGTCAG	2035	
Qy	558	Leu	GlyAsnLeuLeuAlaSerHisIleValThrValHisThrGlyGluLeuProTyrArgCyaaAsn	577
Db	2036	TATTCACATCTTGTAGGGCATCGCAAGAGTTCACTCTGAGAGAAACCATACAAATGTCAT	2095	
Qy	578	Ile	CysGlyAlaGlnPheAsnArgProAlaAsnLeuLeuSerHisThrArgHisSer	597
Db	2096	GAATGTGGCAAAAGCCTTTAATCAGGGCTCCACACTCAATAGACATCAGAGAAATTCATACC	2155	
Qy	598	Gly	GluLeuProTyrLeuCyaaLeuThrCysGlyAlaIaArgPheValGlnValAlaHisIleLeu	617
Db	2156	GGAGAGAAACCTTCAAAATGCATCAAGTGTGGAAATTCCTTAATCAGCGTGCATCTT	2215	
Qy	618	Arg	IaHisValLeuIleHisThrGlyGluLeuProTyrProCysGluIleCysGlyThr	637
Db	2216	AGACTTCATCAGACTGTCATCTACGAGACAGACCTTACAAATGATTAATGAGTGGCAAA	2275	
Qy	638	Arg	PheArgHisIleLeuGlnThrLeuLeuSerHisIleLeuArgHisThrHisThrGlyGluLeu	657
Db	2276	ACCTTTAAACGAGACTCAACCTTCACCTGCATCAGATGAATTAATTCAGCAGAAAGAAACCA	2335	
Qy	658	Tyr	HisCysGlyLeuCyaaAsnLeuHisPheArgHisIleLeuSerGlnLeu-----	673
Db	2336	TATTAAGTGTGAATGTGGCAAGGTATCTCAGGCAATGTTCACTTTGTAAATCACCAG	2395	
Qy	674	Arg	LeuHisIleLeuArgGlnLeu 680	
Db	2396	AGAAATCCACACTGAGAGAA 2416		
RESULT 9				
	US-11-072-512-622			
	Sequence 622, Application US/11072512			
	Publication No. US2006029945A1			
	GENERAL INFORMATION:			
	APPLICANT: ISOGAMI, TAKAO			
	APPLICANT: SUGIYAMA, TOMOYASU			
	APPLICANT: OTSUKI, TETSUJI			
	APPLICANT: WAKAMATSU, AI			
	APPLICANT: SATO, HIROYUKI			
	APPLICANT: ISHII, SHIZUKO			
	APPLICANT: YAMAMOTO, JUN-ICHI			
	APPLICANT: ISONO, YUTKO			
	APPLICANT: HIO, YURI			
	APPLICANT: OTSUKA, KAORU			
	APPLICANT: NAGAI, KEIICHI			
	APPLICANT: IRIE, RYOTARO			
	APPLICANT: TAMECHIKA, ICHIRO			
	APPLICANT: SEKI, NAOHICO			
	APPLICANT: YOSHIKAWA, TSUTOMU			
	APPLICANT: OTSUKA, MOTOYUKI			
	APPLICANT: NAGAHARI, KENJI			
	APPLICANT: MASUHO, YASUHIKO			
	TITLE OF INVENTION: Novel full length cDNA			
	FILE REFERENCE: 084335-0191			
	CURRENT APPLICATION NUMBER: US/11/072, 512			
	CURRENT FILING DATE: 2005-03-07			
	PRIOR APPLICATION NUMBER: US 60/350, 978			
	PRIOR FILING DATE: 2002-01-25			
	PRIOR APPLICATION NUMBER: JP 2001-379298			
	PRIOR FILING DATE: 2001-11-05			
	NUMBER OF SEQ ID NOS: 4096			
	SOFTWARE: PatentIn Ver. 2.1			
	SEQ ID NO: 622			

SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 1778  
 LENGTH: 2110  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-11-072-512-1778

## Alignment Scores:

Pred. No.:	166-21	Length:	2110
Score:	468.50	Matches:	91
Percent Similarity:	48.4%	Conservative:	27
Best Local Similarity:	37.3%	Mismatches:	87
Query Match:	12.4%	Indels:	39
DB:	9	Gaps:	4

US-10-755-889-18 (1-706) x US-11-072-512-1778 (1-2110)

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Qy 472 ProProlyscysThrsercysgllyserglinsrproglinhlsaglmetcysleuhs 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 932 CCTCAAAATGTGAAGATGTGGAAAGCCTTTAACGATTTCTCAATCTTACTACACAT 991
Qy 492 Thr-----AlaglyProThrPhelaaglmetgllyglu-----Thr 504
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 992 AAAAATTCATCTGAGAGAACCTTACATATGTGAAGATGTGGCAAGCCTTTTACC 1051
Qy 505 GluSerGlu-----TyrSerAsp 510
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1052 CAATCTCAACCTTACTACATTAAGAAATTCATCTGAGAAACCTTACCAATGT 1111
Qy 511 SerSerCysgluaengly----- 516
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1112 GAAGAATGTGAAGAAGCTTTTAACCGATCTCAAACTTACTGAACATTAACATTCAT 1171
Qy 517 -----AlaPhePheCysasnGluCysAspCysArgPheSerGluGluAlaSer 532
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1172 ACTGAGAGCAACCTCAAAATGTGAGGAATGCGCAAGCCTTTTAACCGATCTCAAT 1231
Qy 533 LeuLysArgHisThrLeuGlnThrHisSerAspLysProTyrLysCysAspArgCysGln 552
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1232 CTTCAGGAACATGAGAAATTCATACCGAAGAAACCTTCAAAATGTAAAGAAATGTGCC 1291
Qy 553 AlaSerPheArgTyrLysGlyAsnLeuAlaSerHisLysThrValHisThrGlyGlyLys 572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1292 AAAGCTTTAAACATCTCTCAACCTTACTACATTAAGAAATTCACATCTGAGAGAAA 1351
Qy 573 ProTyrArgCysAsnLysCysGlyAlaGlnPheAsnArgProAlaAsnLeuLysThrHis 592
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1352 CCTCAAAATGTGAAGATGTGGCAAGCCTTTTAACCGATCTCAAACTTACTGAACAT 1411
Qy 593 ThrArgLysHisSerGlyGlyLysProTyrLysCysGlnThrCysGlyAlaArgPheVal 612
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1412 AAGAACTCTCACTGGAAGAAACCTTCAAAATGTGAAGATGTGGCAAGCCTTTTATC 1471
Qy 613 GlnValAlaHisLeuArgAlaHisValLeuLeuHisThrGlyGlyLysProTyrProCys 632
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1472 CAATCTCAAACTTACTGAAACATTAATAAAATTCATTTCTGAGAGATACCTTCAAGGT 1531
Qy 633 GluLysCysGlyThrArgPheArgHisLeuGlnThrLeuLysSerHisLeuArgLysHis 652
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1532 GAAGAATGTGCAAGCCTTTTAACATCTTCATCTTACTACATTAATAAAGATTCAT 1591
Qy 653 ThrGlyGlyLysProTyrHisCysGlyLysCysAsnLeuHisPheArgHisLysSerGln 672
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1592 ACTGGGAGAAACCTTACAAATGTGAAGATGTGGCAAGCCTTTTATGCGGATCTCAAAA 1651
Qy 673 LeuArgLysHis 676
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1652 CTACTGAACAT 1663

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RESULT 8  
 US-11-072-512-967  
 Sequence 967, Application US/11072512  
 Publication No. US20060029945A1

## GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO  
 APPLICANT: SUGIYAMA, TOMOYASU  
 APPLICANT: OTSUKI, TETSUJI  
 APPLICANT: WAKAMATSU, AI  
 APPLICANT: SATO, HIROYUKI  
 APPLICANT: ISHII, SHIZUKO  
 APPLICANT: YAMAMOTO, JUN-ICHI  
 APPLICANT: ISONO, YUUKO  
 APPLICANT: HIO, YURI  
 APPLICANT: OTSUKA, KAORU  
 APPLICANT: NAGAI, KEIICHI  
 APPLICANT: IRIE, RYOTARO  
 APPLICANT: TAMECHIKA, ICHIRO  
 APPLICANT: SEKI, NAOHICO  
 APPLICANT: YOSHIKAWA, TSUTOMU  
 APPLICANT: OTSUKA, MOTOMYUKI  
 APPLICANT: NAGAHARI, KENJI  
 APPLICANT: MASUHO, YASUHIKO  
 TITLE OF INVENTION: Novel full length cDNA  
 FILE REFERENCE: 084335-0191  
 CURRENT FILING DATE: 2005-03-07  
 PRIOR APPLICATION NUMBER: US 60/350,978  
 PRIOR FILING DATE: 2002-01-25  
 PRIOR APPLICATION NUMBER: JP 2001-379298  
 PRIOR FILING DATE: 2001-11-05  
 NUMBER OF SEQ ID NOS: 4096  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 967  
 LENGTH: 3026  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-11-072-512-967

## Alignment Scores:

Pred. No.:	3.55e-21	Length:	3026
Score:	465.50	Matches:	178
Percent Similarity:	40.1%	Conservative:	98
Best Local Similarity:	25.8%	Mismatches:	238
Query Match:	12.3%	Indels:	179
DB:	9	Gaps:	27

US-10-755-889-18 (1-706) x US-11-072-512-967 (1-3026)

```

Qy 84 CysLleuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGlyAsn---Ile 102
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 609 TGCCCATGTGAAGAAACATCTTACTGTGTAAGAAAGATCAACATGTCAGAGGAGATGAGAAA 668
Qy 103 MetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValValaPheThrCysArg 122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 669 ACAATCTATTTGAAACACAGCTTACATCAAACTTTGAGTCAACGCTGCGTGAACCTGAGA 728
Qy 123 LysPheLysLeuValaSerGluValaGluMetValaSerLysLeuLysProProArgGluGlu 142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 729 AAGTTT-----AACTGGAAGGAGACTTATGAAATGTAATGAAGAAACGAGAGACAGATA 782
Qy 143 -----PheLeuAsnSerArgMetLeuMetProGlnaAspIleMetAlaTyr 157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 783 ATAAATGTTGTTAGTTTCACACACA-----TTAGGAGAAA 818
Qy 158 ArgGlyArgGluValaGluAsnLeuProLeuArgSerAlaProGly----- 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 819 AAAGGTATGTATGTAAGATGTGGCAAGCCTTTAAAGCCTTCCAGCTTATTAATC 878
Qy 175 CysGluSerArgAlaPheAlaProSerLeuTyrSerGlyLeuSerThrProPro----- 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 879 ATCAGAGATACATACAGAGAAACCTTACAAATGAATGAATGTGGCAAGCCTTTC 938
Qy 193 -----AlaSerTyrSerMetTyr-----SerHisLeuPro 202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 939 ATCGGCTCTCACTACTACTGATACCAAGATGTCATACAAAGAGAAATCATATCATAT 998

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; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2436

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Alignment Scores:

Pred. No.:	6,59e-22	Length:	157e
Score:	472.50	Matches:	143
Percent Similarity:	39.8%	Conservative:	53
Best Local Similarity:	29.1%	Mismatches:	199
Query Match:	12.5%	Indels:	98
DB:	12	Gaps:	16

US-10-755-889-18 (1-706) X US-11-136-527-2436 (1-1578)

Oy	197	MetTrYSerHISLeuProValSerSerLeuLeuPheSerAArgLIGluPheArgAspVal	216
Db	349	ATGTTGGAAAGCGCTTACGCCGAGTCAGAGCTTCTGCATGATGAA-----	393
Oy	217	ArgMetProValAlaAsnProPheProLysGluArgAlaLeuProCyAspSerAlaArg	236
Db	394	-----CCTGATCCTCGAGAGAAAGTTATGTAATGATGATGATGAG	435
Oy	237	ProValProLysGluTrYSerArgProThrLeuGluValSerProAlenValCysHisSer	256
Db	436	AAAAAC-----TTTAGCCTAGAACACACTTTGTGGAAACATTAAGAAAACCCAGGT	486
Oy	257	AsnIleTrYSerProLysGluThrIleProLysGluAlaArgSerAspMetHisTrYSer	276
Db	487	GGG-----GAGAGTCACCCGAGTGTACCGGATGTGCGTAGAGATTTCCG	531
Oy	277	ValAlaGluGluLeuLysProAlaAlaProSerAlaArgAlaAlaProTrYPheProCyS	296
Db	532	AAAGCGCTTCACTTACTGCAATCTGAGAGAGCGCTTCCAGGAGGAGATCATTAATAGT	591
Oy	297	AepLysAlaSerLysGluGluGluArg-ProSerSerGluAspGluIleAlaLeuHisIspH	316
Db	552	GGTAACTGTGG-----AGAACCTTACCCAGAGAGAAACTTCC-----TT	633
Oy	316	eglUProPheAlaAlaProLeuAsnArgLysGluLeuValSerProGlnSerProGlnLys	336
Db	634	TCTCAGCAGAAACATCATGCTGAAAGA-----GACCCAGAGATCTTAAGAA	681
Oy	336	S-----SerArgCysGlnProAsnSerProThrGluAlaCysSerSerLysAsnAlaCys	354
Db	662	ACTCCCGTCCCATGACACCATCTGTCCAGAAATCAGAGAAACCCGGAGATTAACCATAT	741
Oy	354	glleuGlnAlaSerGlySerProProAlaLysSerProThrAspProLysAlaCysAs	374
Db	742	CGGTGTAGAGACTGTGGAAAGCT-----	766
Oy	374	nTrpLysLysTrpLysPheIleValLeuAsnSerLeuGlnAsnAlaLysProGlyGlu	394
Db	767	-----TTAATGGCAAAATCATATCTCAAAAGAACATGAGAAATAATTCAT	807
Oy	394	yProGluGlnAlaGluLeuGlyArgLeuSerProArgAlaTrpThrAlaProAlaCys	414
Db	808	ACCGGAGAGAAACCATTTGAATGTATACGT-----GTGGTAGAGCTTTCAGC	855
Oy	414	eglInProMetGluProGluAsnLeuAspLeuGlnSer-----ProThrLysLe	431
Db	856	CAGAGACAGTACTCATTT-AAACACACAGAACCTGCACAGTGGAAGAAAGCCTTTAAATGTG	914
Oy	431	userAlaSerGlyGluAspSerThrIleProGlnAlaSerArgLeuAsnAsnAlaIleVal	450
Db	915	TAATAGTGTGTGAAG-----GCTTTAGCCAGAAAGAAACCTATATAT	959
Oy	451	-----AsnArgSerMetThrGlySerProArgSerSerGergLysSerHisSerProLeuTrp	469
Db	960	ACACCGAGAAATCCATACCGGAGAG-----	984
Oy	469	trMetHisProProLysCysThrSerCysGluLysGlnSerProGlnHisAlaGluMetCys	489
Db	985	---AAGCCTTATGAATGTAAAGGGGTGGAAAGCCTTCATTCAGAAATCAAGCCTCAT	1049

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Oy 489 sLeuNIsthrIaGLyProthPhealIaGLuImeGIlVgIuthrgInserGIuTyse 509
Db 1041 CAGACACAGAGAGGCCATACT-----GGAGAGAA----- 1071
Oy 509 rAsPserSerCySGluabngIyLaPhePheCyvaSngIuCyvaSPCyarGPheserGI 529
Db 1072 -----CCGTACACATTTAGAAAGATGTGGAAAGCCCTTCAGCGG 1109
Oy 529 uGIuIaSerIeulYsaRhIsthrIeugInthrhIsearIySProTyTlyvCyvaS 549
Db 1110 CAAATCAAACTGACTGAGCATGAGAAATTCATATTGGAGAAACCTTTAAATGTAA 1165
Oy 549 pArGcySGIaIaSerPhearGTYTlyvSGIYasIleuIaSerIstlyvthrValIstH 569
Db 1170 CGAGGTGGAAACAATTTTCAGGCAAGAGACGTACTCTCAACAATCACAACATTCCAC 1223
Oy 569 rGIvGIuIvProTyTArGcyvaSngIleCySGIYalagIaPhevaIaGrProIaasIle 589
Db 1230 GGGCGAAGGCCATrTAGTGCATTAATGTGGAAAGCCCTTTGTGAAATCAGTGCT 1288
Oy 589 uLySThrthIsthrIaGLIehIseRGIyGLuYvProTyTlyvCySGIuThrIcySGIYal 609
Db 1290 TATTGTGCATGTGAATTCACACAGGGGATAAACCCCTATAGAGTAAAGTGTGGGAA 1349
Oy 609 aArGPhelalGInIaIaIaIstlyeuaTgAlaIaIstValIeulIehIsthrGIyGLuYvPr 629
Db 1350 AGCCTTCTGTAGAGTTCGCTTCACCCGTGCATrTAGAGGACCCACAGGGTGAAGAAC 1405
Oy 629 cTyTProCySGIuIleCySGIYThrArGPhearGHIstleuGIInthrhIeulYvSerIaIe 649
Db 1410 GTATGCGTGCATAGTGTGTGGAAAGGCTTTTTCAGATGTTCACCTGTGCTTAAACAT 1465
Oy 649 uArGIleIsthrGIyGLuYvProTyTThIsCySGIuYsCyvaSngIeulIstPhearGHI 669
Db 1470 GAGAAATCACACTGGCGAGAAAGCCTTAACTAGTGAAGTGTGGAAAGCCCTTCAGCCA 1525
Oy 669 sLyseSerIIneuarGleuHIstlyeuaTgGInly 680
Db 1530 GAAATCCAT-----CACTATAGCACACAG 1554

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## RESULT 7

```

US-11-072-512-1/78
Sequence 1778, Application US/11072512
Publication No. US20060029945A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHITO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOHYUKI
APPLICANT: NAGAHARA, KENJI
APPLICANT: MASUHO, YASUHIKO

TITLE OF INVENTION: Novel full length cDN
FILE REFERENCE: 08435-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096

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Pred. No.: 1.16e-21 Length: 3090  
 Score: 473.00 Matches: 165  
 Percent Similarity: 40.0% Conservative: 68  
 Best Local Similarity: 28.4% Mismatches: 200  
 Query Match: 12.5% Indels: 150  
 Gaps: 28

US-10-755-889-18 (1-706) X US-11-072-512-191 (1-3090)

QY 182 ProSerLeuTyrsSerGlyLeuSerThrProProAlaSerTyrsMetTyrsMetLeu 201  
 Db 519 CCATCGATG---TCAGATCCACACACCTGGCTGAT----- 554  
 QY 202 ProValSerSerLeuLeuPheSerAspGluGluPheArgAspValArgMetProValAla 221  
 Db 555 -----GATTCCTCTGCTCTTCA-----GAGTTTGG-GATATGAGATGAAAAATGAC 601  
 QY 222 AsnProPheProGlyArgGluAlaLeuProCyAspSerAlaArgProValProGluGlu 241  
 Db 602 ACTCGGAATTTCTCTGAGAGAGAGTACCTGTGATGA-----GAA 643  
 QY 242 TyrsArgProThrLeuGluValSerProAsnValCyHisSerAsnIleTyrsSerPro 261  
 Db 644 GTGGAAAGATTCAACAGGGAAGTCCC-----TGCTGTCCAGTTTAAAGTGATGAT 694  
 QY 262 LysGluThrIleProGluGluAlaArgSerAspMetIleTyrsSerValAlaGluGlyLeu 281  
 Db 695 TGGGACGT-----GAGAACCCAGAGGAGACCTTGAGGCACCTTAACCTCTGGAG 748  
 QY 282 LysProAlaAlaProSerAlaArgAsnAlaProTyrsPheProCyAspLysAlaSerLys 301  
 Db 749 AAACCAAGGACTCAGGAAGCA-----ATTGTGAATATCCGTGTTT 790  
 QY 302 GluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAsnAla 321  
 Db 791 GGGAGGACTTGTGATGGCAAGCTCAGAC-----CTTCCACCTCTCAGAGCA 835  
 QY 322 ProLeuAsnArgLysGlyLeuValSerProGlnSerProGlnLysSer---AspGln 340  
 Db 836 GTTCTGGCAACAAATGGTTTCCATGACCTGACTCAATGTTAGTGGTGGATGGATGAC 895  
 QY 341 ProAsnSerProThr-----GluAlaCySerSerLysAsnAla 353  
 Db 896 CCCGCTTACCCAGCTATCTTAAAGTTATGACATTAAGAACTCGGAGCAAGTGAATGCC 955  
 QY 354 Cys-----IleGluGlnAlaSerGly-----Ser 361  
 Db 956 TGTGGAAGAAAGCTTCAACCATTCATGAGAGTTATTCATGGAAGAAATCCAGTGAAGAG 1015  
 QY 362 ProProAlaLysSerProThrAspProLysAlaCyAsnTrp----- 375  
 Db 1016 AAGCCTTACCAATACCTCGAAAGTGTTAAGTCTTTTATCATTTTACTCTCTGGTCAT 1075  
 QY 376 -----LysLysTyrs-----Phe 380  
 Db 1076 CAGAAATTAATGAAGAGGCAAGAAATCGATGAAGTAAAGATTGGAACATCTTT 1135  
 QY 381 IleValLeuAsnSerLeuAsnGlnAsnAlaLys-----ProGlyGlyProGluGln--- 397  
 Db 1136 ACTCGAGCTCATGCTTATGATGAAGAAACAGAGAAATCTCCCTGGAGAGAAACAAATATGAG 1195  
 QY 398 ---AlaGluLeuGlyArg-----LeuSerProArgAla 407  
 Db 1196 TGTACTGATGTGGCAAAATGCTTCAACGGAATCTTCTCTGTTTTCATCACCAGACT 1255  
 QY 408 TyrThrAla-----ProProAlaCyGlnPro-----PrometGluProGluAsnLeu 423  
 Db 1256 CACACCGGAGAGAGAGCCTTATATCTGTATAGTGTGAAAGCTCTTCTCCAGAGATAC 1315  
 QY 424 AspLeu-----GlnSerProThrLysLeuSerAlaSer 434  
 Db 1316 AACCTGATTTGTCATCAAGATCCACACAGAGAGAAAGCCCTATGAATGCGTAAATGT 1375

QY 435 Gly-----GluAspSerThrIleProGlnAlaSerArgLeuAsnIleVal 450  
 Db 1376 GGGAAAGCTTTCAGTATGAGCTCAGCTGACACACACAGCAAGAAATTTTCA----- 1426  
 QY 451 AsnArgSerMetThrGlySerProArgSerSerSerGlnSerHisSerProLeuTyrsMet 470  
 Db 1427 -----ACAGCCGAG----- 1435  
 QY 471 HisProProLysCySerThrSerCyGlySerGlnSerProGlnHisAlaGluMetCyLeu 490  
 Db 1436 AAACCTTATGAATGCCATGAGTGTGAAAAACCTTCAACGGAATATCATCTTAATTTTG 1495  
 QY 491 HisThrAlaGlyProThrPheAlaGluGluMetGlyGluThrGlnSerGluTyrsSerAsp 510  
 Db 1496 CACCAAGAAACATATCA-----GGGAAAAA----- 1522  
 QY 511 SerSerCyGluAsnGlyAlaPhePheCyAsnGlnCyAspCyAspArgPheSerGluGlu 530  
 Db 1523 -----CCATATGATGTACGAATGTGGAAACCTTCACTGACATC 1564  
 QY 531 AlaSerLeuLysArgHisThrLeuGlnThrHisSer---AspLysProTyrsCyAsp 549  
 Db 1565 TCCACCTTCACTGATGAT---CTCAGAAATCACAACCGGTGAGAAAGCCCTATGATGATGAC 1621  
 QY 550 ArgCyGlnAlaSerPheArgTyrsGlyAsnLeuAlaSerHisLysThrValHisThr 569  
 Db 1622 AAATGTGAAAGGCTTTCCGGAAGGCTGCTGACTCACCCAGCATGAGAGACTCACACT 1681  
 QY 570 GlyGluLysProTyrsArgCyAsnIleCyGlyAlaGlnPheAsnArgProAlaAsnLeu 589  
 Db 1682 GGAAGAAAGCCCTTGAAGTGTGACAGTGTGGGAAATCTTCAACAGAAATCTCACCTC 1741  
 QY 590 LysThrHisThrArgIleHisSerGlyGlyLysProTyrsCyGluThrCyGlyAla 609  
 Db 1742 ATTGTGCATCAAAAGATTCATTTCTGGAGAAACCTTGAATGAATGAATGCGCAAG 1801  
 QY 610 ArgPheValGlnValAlaHisLeuArgAlaHisValLeuIleHisThrGlyLysPro 629  
 Db 1802 ACTTTCATCGAAGAGTGGTACTCATCAGGACATCAGAGATTCATCTGCGAGAAACCC 1861  
 QY 630 TyrProCyGluLysLeuGlyThrArgPheArgHisLeuGlnThrLeuLysSerHisLeu 649  
 Db 1862 TATGCTGCAACCAAGTGTCAAGAACTTTTCAAGAAATGCTGCGCTCATTTAGGACACAG 1921  
 QY 650 ArgIleHisThrGlyGlyLysProTyrsHisCyGluLysCyAsnLeuHisPheArgHis 669  
 Db 1922 AGACATCATCTGTGAGAAAGCCTATGAGTGAATCAGTGTGGCAAAAGCTTCAAGGAC 1981  
 QY 670 LysSerGlnLeu-----ArgLeuHis-LeuArgGlnLysHisGlyAlaIleThr 685  
 Db 1982 AGCTTCCTGTCTGACCAAGCAGCAGCAAGATTCACCTAAAGAGACCCCATATCAGTGTCCA 2041  
 QY 685 rAsn 686  
 Db 2042 GAAT 2045

RESULT 6  
 US-11-136-527-2436  
 ; Sequence 2436, Application US/11136527  
 ; Publication No. US20050287570A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Mount, William M  
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
 ; FILE REFERENCE: 031896-041000 (AM101086)  
 ; CURRENT APPLICATION NUMBER: US/11/136,527  
 ; CURRENT FILING DATE: 2005-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/574,294  
 ; PRIOR FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 362830  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 2436  
 ; LENGTH: 1578

```

Db      1002 ----GCTGTGTTGTTCCACCCAGAGAAATGGTGTGTTCTGACTCTACTCAGAGAGCCT 1057
Qy      213  -PheArGPValArgMet-----ProValAlaAspProPheR 225
Db      1058  GATATAGATGTGATGCTGTGAGAACTACAGAACTGGGCTGTGGCTGATGCACTGG 1117
Qy      225  oLygIuArGAlaLeuProCyAspSerAlaArgProValProGlyIuLyTyrSerArgPr 245
Db      1118  CAATCCAAATGGCTGTCTTATTTGAGAAAGA-----GGAGACAGTGGACAC 1168
Qy      245  oThrLeuGluValSerProAsnValCyHisSerAsnIleTyrSerProGlyIuThrI 265
Db      1169  TGACAGAGGGCGTCTCTCAGACACCTGTGCAGAACTCAGTGTCAAACCCAGAGGCAAT 1228
Qy      265  eProGluIuAlaArgSerAspMetHisTyrSerVal---AlaGluGlyLeuIuProAl 284
Db      1229  TCTTAGCCAAAGTACTTTTACAGAGATCCGTGCTCATGTGATGTAAGGAGGAGCAACT-- 1286
Qy      284  aAlaProSerAlaArgAsnAlaProTyrPheProCyAspIyAlaSerIyGluIuGl 304
Db      1287  -CAGCCTGAGAGAAATCTATATATATATGAACTTGAGAAACCTTTTAAACAGCATTA 1345
Qy      304  uArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAsnAlaProLeu 324
Db      1346  ACCACTTTTCCAGTACCAAGAAATTCATGCTGAG-----AGGCATCTGTGA 1393
Qy      324  snArgIyGlyLeuValSerProGluIuSerProGluIuSerAspCyGluIuProAsnSer 344
Db      1394  ATCTCAAGAGATTAGAAATTCCTCTTCC-----AGAGTGC 1429
Qy      344  roThrGluAlaCySerSerIyAsnAlaCyAlleuGluAlaSerGlySerProPro 364
Db      1430  CCACCTAATGTGC-----CCGA 1447
Qy      364  lAlaSerSerProThrAspProGlyAlaCyAsnTrpIyIySyrIySyrPheIleValLeu 384
Db      1448  GAAATATCC-----GTAGTGGGAGATTA 1468
Qy      384  snSerLeuAsnGlnAsnAlaIyProGlyIyProGluIuAlaGluLeuIyArgLeu 404
Db      1469  AT----- 1470
Qy      404  eProArgAlaTyrThrAlaProProAlaCyGlnIuProPoweGluProGluIuAsnLeu 424
Db      1471  -----CCTATGATGTAACAATGTGA 1492
Qy      424  sPleuGlnSerProThrIyIuSerAlaSerGlyIuAspSerThrIleProGluAla 444
Db      1493  AAAATCTTCAATACAGCTGTGACCTTATCAGAGCATGAGAGATCATATCTCAGAGAA 1552
Qy      444  eArgLeu-----AsnAsnIleValAsnArgSerMetThrGlySerProArgSerSer 462
Db      1553  GTCTTTGACTGTCAAGAAATGTGGGCAAGCTTCA-----AATATCTCTCGAATCTCCG 1606
Qy      462  eArgIuSerHisSerProLeuTyrMetHisProPro---IySyrIuSerCyGlySerG 481
Db      1607  GCGACACATGAGAAACCATATACC-GGAGAGAAAGCATTTGATGATAGCACTGTGGGAAA 1665
Qy      481  InSerProGlnHisAlaGluMetCyIleuHisThrIleArgIyProThrPheAlaGluIu 501
Db      1666  CCTTCAGAGAACTTAACTGATTTTGCACAGAGAAACACACA----- 1712
Qy      501  eArgIuIuThrGlnSerGluTyrSerAsp-----SerSer 513
Db      1713  --GAGAGAGAGCCCTACAGATGTAAAGATTGTGGAAAGCCTTCAATCAGCANTCACC 1770
Qy      513  yGluIuAsnGlyAla-----PhePheCyAsnGluCyAspC 525
Db      1771  TCAGAGACCAAGTGAAGTCACTGAGAGAGAGCCCTTGAATGACAGCAGTGTGGGA 1830
Qy      525  yArgPheSerGluIuAlaSerIleuIyArgHisThrLeuGlnThrHisSer---Asp 544
Db      1831  AAGCTTTCAGAGAACTTCACTTCACTGAAGACAT--CTGCGAAACCATACAGAGAGA 1887

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Qy      544  yProTyrIyCyAspArgCyGlnAlaSerPheArgTyrIyGlyIuAsnLeuAlaSerH 564
Db      1888  AACCATATGAAATGCAACAGATGTGGCAAGCCCTTCCGACGACACTCATCTGAACGTGC 1947
Qy      564  lAlaValHisThrGlyIuIyPProTyrArgCyAsnIleCyGlyAlaGlnPhe 584
Db      1948  ACAAGAGATACACAGAGGAGAAATCTATAGATGTGGCGGCACTTGGCTCAGCTTCA 2007
Qy      584  snArgProAlaAsnLeuIyThrHisThrArgIleHisSerGlyIuIyPProTyrIyG 604
Db      2008  GTGCTTTTCAACCTTGAAGAGTGCATGCGAACTCACACTGAGAGAAAGCCCTATGTGT 2067
Qy      604  yGluIuThrCyGlyAlaArgPheValGlnValAlaHisIleuArgAlaHisValLeuIleH 624
Db      2068  GCCAGAAATGTGGGAGAGCCTTCACTGAGCCCTCATCTCCCTGAGAAACATGCAAGAGATC 2127
Qy      624  lThrGlyIuIyPProTyrProCyGluIleCyGlyIuThrArgPheArgHisLeuGlnT 644
Db      2128  ACAGTGGCAAGAGCCCTATGATGATCCAGAAATGGCGGAGCCCTTGTGCTAGTTCAC 2187
Qy      644  hrLeuIySerHisIleuArgIleHisThrGlyIuIyPProTyrHisCyGlyIuIyCy 664
Db      2188  ATCTTATTGTACATGTGAGAACACACAGTGCAGGAGACCTTATCAATGTAATCAGTGTG 2247
Qy      664  snLeuHisPheArgHisIySerSerGlnLeuArgLeuHisIleuArgGlnIyHisIyAla 684
Db      2248  AGAAAGCCCTTCAGGACAGCTCTTCACTCATGTACACAAAGAACCCATGTGGAGAG 2307
Qy      684  lThr 685
Db      2308  AGACC 2312

```

```

RESULT 5
US-11-072-512-191
; Sequence 191, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 08435-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 191
; LENGTH: 3090
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-072-512-191

```

Alignment Scores:

```

Db      797 ATGATGCTGTGTGAAAAAACCTTCATTAAACACTATCCCTTGTAACATGAGAAAAA 856
Qy      392 ogylylProgluIn-----
Db      857 CCATAGTGGAGAGAAACCTATTAGTGAAGATGTTCAAAAGCCTTAGCCAAAGTTC 916
Qy      398 -----AlaGluLe 400
Db      917 AGCTTATTTCACATAATACACACTACTGGAGAGAAACCTTACATATGTAAAGAAATG 976
Qy      400 uGlyArgLeuSerProArGAlaYrThrAlaProProAlaCyGSluInProFowetGluPr 420
Db      977 TGGG-----AAAGCCTTACTCTCAGTACATCCCTTATAAAGCTTAAGAAC 1024
Qy      420 oGluAsnLeuAspLeu-----425
Db      1025 CCATACCTGTGAGAAATCTTACAGATGTAAAGAAATGTGTAAATCCTTACAGCCGAGGTC 1084
Qy      426 -----GluSerProThrIysLeuSer-----432
Db      1085 AGGCTTTTATACATCAAAAAATTCATGCTGAAGAAACCTTGTAAATGTATATCCGGG 1144
Qy      433 -----AlaSerGlyGluAspSerThrIleProGlnAlaSerArgLeuAsnAlaIva 450
Db      1145 TAGGAAGGATCTAGTTGCACACATCCCTTTCGATGTCAAGAAATTCATTCTAGAAA 1204
Qy      450 lAsnArgSerMetThrGlySerProArgSerSerGluSerIserProLeuYrme 470
Db      1205 GAAGTCTCTATTATGTATGAATGTGGCAACCTTAAAGCTTAACTCATCCCTTCGTTA 1264
Qy      470 tHis-----ProProLysCySerHisCyGSluSerGlnSe 482
Db      1265 TCATCAAGAAATTCACACTGGAGAGAACCTTTTAAATGTAAATGTGAATGTGAGAGCCTT 1324
Qy      482 rProGlnHisAlaGluMetCySLeuHisThrAlaGlyProThrPheAlaGluGluMetG1 502
Db      1325 CAGCGAGAGTCCCTCTCTTATTCAACAT-----GAAAGAAATTC 1363
Qy      502 yGluThrGlnSerGluYrSerAspSerSerCyGSluAsnGly-----516
Db      1364 CACCGAGAAAGCCCTATAGATGCAATGATGTGGAAAGCCTTACTTCAATTCACG 1423
Qy      517 -----AlaPhePheCyAsnGluCyAs 524
Db      1424 ACTTAATAGACACCGAATCATTCATATCTGAGAGAAAGTATTAATTAATGATGTGG 1483
Qy      524 pCyAsArgPheSerGluGluAlaSerLeuIysArgHisThrLeuGlnThrHisSerAspLy 544
Db      1484 TAAAGCCTTAAGCTCCCACTCAACACTTATTATTCACAGAGGAATTCATCTGAGAGAAA 1543
Qy      544 sProTyxIysCyAsArgCyGlnAlaSerPheArgTyxIysGluAsnLeuAlaSerHis 564
Db      1544 ACCATGTAAATGTAAAGTATGTGAAAAAGCCTTCAAGACAGATTCAGCTCATTCACAA 1603
Qy      564 slySerThrValHisThrGlyGluYrProTyxArgCyAsnAlaIleCyGSluAlaGlnPheAs 584
Db      1604 TCAGAGAAATGCACTACTGAGAGAAAGCCCTATTAAGTAAACAGATGTGGAGAAAACTTAG 1663
Qy      584 nArgProAlaAsnLeuIysThrHisThrArgTlleHisSerGlyGluYrProTyxLeuCy 604
Db      1664 GTGTAACTCATCATTAAGTAAATCACCAGAGAAATTAATCTGAGAGAAACCTATTCAGATG 1723
Qy      604 sGluThrCyGSluAlaArgPheValGlnValAlaHisIleuArgAlaHisIvalLeuIleHis 624
Db      1724 TGAGGAATGTGGGAATCTTTTGGCAAAAGTTCACACTCTTATTACAGATTCGAAGATTC 1783
Qy      624 sThrGlyGluYrProTyxProCyGSluIleCyGSluYrThrArgPheArgHisIleuGlnTh 644
Db      1784 TCACAGAGAGAAAAACCTTTAAATGTAAATCAGATGTGAGAAAACTTTAGCAAAAGCTCATC 1843
Qy      644 rLeuIysSerHisIleuArgTlleHisThrGlyGluYrProTyxHisIleuCyGSluYrCyAs 664

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Db      1844 ACCTATTGCACATCAGAGAAATTCATATCTGAGAGAAACCTTATGAATGTAAATCATGTGG 1903
Qy      664 nLeuHisPheArgHisIleuSerGlnLeuArgLeuHisIleuArg 678
Db      1904 GAAACTTTTCAACCATTAAGTGATCCCTTACTATCATTTATAA 1946

RESULT 4
US-11-072-512-1944
; Sequence 1944, Application US/11072512
; Publication No. US2006002945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: MAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUDKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: INIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SERI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072, 512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350, 978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1944
; LENGTH: 2784
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-1944

Alignment Scores:
Pred. No.: 8,39e-22 Length: 2784
Score: 474.50 Matches: 167
Percent Similarity: 39.6% Conservative: 72
Best Local Similarity: 27.7% Mismatches: 228
Query Match: 12.5% Indels: 137
Gaps: 21

US-10-755-889-18 (1-706) x US-11-072-512-1944 (1-2784)
Qy      130 AlaGluMetValSerAlaIleIleYrProProArgGluGluPheLeuAsnSer-ArgMetLe 149
Db      776 GCCGCCCTTGCTCTGCGGATGACGAGGACGGAAGCCGCTATGCAAGATTCGAGAGGTGCT 835
Qy      149 uMetProGlnAspIleMetAlaYrArgGlyArgGluValAlaGluAsnAen---LeuPr 168
Db      836 GATACCACTGCTTACACTGGGCCACCGCAACCCATGGGTGCGCAGAGATTCGTGCTGTGCC 895
Qy      168 cLeuArg-----SerAlaProGlyCyGSluSerArgAlaPheAlaProSe 183
Db      896 TGCAAGTACACCTGCTGCTTTCAGAGAGCAAAAGTGGAGGAAGAAAGCTATGCTGTGG 955
Qy      183 rLeuTySerGlyLeuSerThrProProAlaSerTySerMetTySerHisIleuProVa 203
Db      956 GCTGCAACCGCCCTGTTTCACAGAAACAGTCACTTTCAGATGTG-----1001
Qy      203 lSerSerLeuAspPheSerAspGluGlu-----212

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1413 AGGATCCACAGGGT----- 1427
1426 GlnSerProThrLysLeuSerAlaSerGlyGluAaspSerThrLeuProGlnAlaSerArg 445
1428 GAGAGCCCTTAATTAATGTGAGAAATGTGTAAAGGCTTCACT-----CAGCTGCACAT 1481
446 LeuAsnAsn1LeuAlaAsnArgSerMetThrGlySerProArgSerSerGlu----- 463
1482 TTT---CACATTCATCAGAGAGTCCACATCTGAGAGAAACCTTACAAAGTGTATGTGTGT 1538
464 -----SerLeu---SerProLeuTyMetHis----- 471
1539 GGTAAAGGCTTCAGCCCAATTCACATTAATATGTCAGAGAGTCCACAGAGAGAG 1598
472 ---ProProLysSerGlySerGlySerGlnSerProGlnHisAlaGluMetCysLeu 490
1599 AAGCCATACAGTGTAGAGCGGTGTGGAAAGGCTTACCCGTAAATACAGATCTGCATATT 1658
491 HisThrAlaGlyProThrPheAlaGluGluMetGlyGluThrGlnSerGluTySerAap 510
1659 CAT-----TTCAAGATTCCACAGGAGAG-----AAACCTTAATATGT 1697
511 SerSerCysGluAenGly----- 516
1698 AAGAGTGTGTAAAGGCTTCACTCAAGCTTCAATCTTCAAGTCCATCAGAAATGTCCAC 1757
517 -----AlaPhePheCysAsnGluCysAapCysArgPheSerGluGluAlaSer 532
1758 ACTGGGAGAAACGATTCAGATGTGAACGTGTGGAAAGGCTTCACTCACTCACTCAAAAG 1817
533 LeuLysArgHisThrLeuGlnThrHisSerAspLysProGlyLysCysAapArgCysGln 552
1818 CTTCAAAACCATCAGAGAGTCCACACTGAGAGAAACCATATAGATGTATGTGTGTGTGT 1877
553 AlaSerPheArgTyLysGlyLeuLeuAlaSerHisLeuThrValHisThrGlyGlyLys 572
1878 AAGCATTCAGATTATGTTCAATCTTAACTTAACTACACAGTAAATTTCACTGAGAGAAAA 1937
573 ProTyArgCysAsn1LeuGlyAlaGlnPheAsnArgProAlaAsnLeuLysThrHis 592
1938 CCAATTAATGTAGAGAAATGTGGAAAGGCTTCACTGAGAGATCAATCTTCACTGCACAT 1997
593 ThrArg1LeHisSerGlyLysProGlyLysCysGluThrCysGlyAlaArgPheVal 612
1998 CAAGAAGTTCACAGAGAGAAAAACCTTAATATGTGAGAGAGTGTATTAAGAGCTTCAGT 2057
613 GlnValAlaHisLeuArgAlaHisValLeu1LeHisThrGlyGlyLysProGly 632
2058 CAGGCCATAGATTTCGGGTATCATCAGAGAGTCCATATCTGAGAGAGCCATCAATATGT 2117
633 Gln1LeuGlyLysThrArgPheArgHisLeuGlnThrLeuLysSerHisLeuArg1LeHis 652
2118 GGTGTGTGTGTAAAGGCTTCACTCACTCTGTGTGTCAATCTTCACTCACTCACTCACTCA 2177
653 ThrGlyLysProTyArgHisCysGlyLysCysAsnLeuHisPheArgHisLysSerGln 672
2178 ACGGGGAGAAACCATCAATCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2237
673 LeuArgLeuHisLeuArgGlnLysHisGly 682
2238 TTTATATACCATCAGAGAGGCCACACTGGA 2267

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CURRENT APPLICATION NUMBER: US/11/000,688
CURRENT FILING DATE: 2004-12-01
PRIOR APPLICATION NUMBER: US 60/525,987
PRIOR FILING DATE: 2003-12-01
NUMBER OF SEQ ID NOS: 1596
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1136
LENGTH: 2435
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial sequences: primer
NAME/KEY: misc_feature
LOCATION: (1)..(2435)
OTHER INFORMATION: zinc finger protein 354a(ZNF354A) gene..
US-11-000-688-1136

Alignment Scores:
Pred. No.: 6,84e-22 Length: 2435
Score: 475.00 Matches: 152
Percent Similarity: 38.0% Conservative: 82
Best Local Similarity: 24.7% Mismatches: 205
Query Match: 12.5% Indels: 177
DB: 12 Gaps: 16

US-10-755-889-18 (1-706) x US-11-000-688-1136 (1-2435)
205 SerLeuLeuPheSerAapGluLys-----Phe 213
210 GCTGTGTCTTTAATCCGAGATAGTGAGAAAGCTGCCCTTTCAGAGAACTTTGTC 269
214 ArgAapValArgMet-----ProValAlaAsnProPheProLys 226
270 CCGGATGTGATGCTGAGAACTATAGAACTGTCTCACTGAGGCTCCCATTTACCAAA 329
227 GlnArgAlaLeu-ProGlyAapSerAlaArgProValProGlyGlyLysSerArgProth 246
330 CCAAAAGTATCTCCCTGTTGCGAGAGAGAAAGATCCCTGTGAGGTGAGAAAGCGGT 389
246 rLeuGluValSerProAsnValCysHisSerAsn1LeuTySerProLysGlyThrLePr 266
390 TCTGGC-GTCTCCTCTCTAGATCCAGAGAGCTCATTAACCAAAATCAACGCAAC 448
266 oGluGluAlaArgSerAapMetHisTySerValAlaGluGlyLeuLysProAla1a1aPr 286
449 ACAAGAC-----TCTCATTTCAAGGACTG---ATACTGAAGAAG 484
286 oSerAlaArgAsn1a1aProTy----- 293
485 ATCCAAACAGAAATGATCACTTGGATTGAAATTAAGAAAGCCTTACATATATGAAGCAG 544
294 -----PheProCysAapLysAlaSerTySerGluG1 303
545 ATTAGAGAAAAACGAGATTAAGAAAGGAGATTTTCAGATAGTTTCCACCCACCAAAAA 604
303 u-----GluArgProSerSerGlyLysArgGluLeuAlaLeuHisPheGluProPr 319
605 AATCCCACTTAATTAAGAAAGGACATTAATAATCTGAATAGAGCAAAATTCAGCCCAA 664
319 oAsn1a1aProLeuAsnArgLysGlyLeuValSerProGlnSerProGlnLysSerArgC 339
665 GTCAAGTCTTAATTAAGCAACAGATACCTTCCAGAGAAAGAAACCAACCAAAATGTAAAT 724
339 eGlnProAsnSerProThrGluAlaCysSerSerLysAsnAlaCys1LeuGlnAla1a1a 359
725 ACAAGAAACAGC-----CTCAACAGAAATTCACATTTACT----- 761
359 rGlySerProProAlaLysSerProThrAapProLysAlaCysAapTrpLysTyLysTy 379
762 -----AATCAACCAAAATTAACGAGATTAACGCTATATA 796
379 s-----Phe1LeuAlaAsnSerLeuAsnGlnAlaAsn1a1aLysPr 392

```

## RESULT 3

```

US-11-000-688-1136
Sequence 1136, Application US/11000688
Publication No. US20050287544A1
GENERAL INFORMATION:
APPLICANT: BERTUCCI, Francois
APPLICANT: HOUIGATTE, Remi
APPLICANT: BIRNBAUM, Daniel
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
FILE REFERENCE: 1423-R-03

```

QY 701 GlutProlyserAlaCys 706  
 DB 2428 GAGCTCCCAAGGCTTC 2445

## RESULT 2

US-11-072-512-959  
 / Sequence 959, Application US/11072512  
 / Publication No. US200602945A1  
 / GENERAL INFORMATION:  
 / APPLICANT: ISOGAI, TAKAO  
 / APPLICANT: SUGIYAMA, TOMOYASU  
 / APPLICANT: OTSUKI, TETSUJI  
 / APPLICANT: MAKAMATSU, AI  
 / APPLICANT: SATO, HIROYUKI  
 / APPLICANT: ISHII, SHIZUKO  
 / APPLICANT: YAMAMOTO, JUN-ICHI  
 / APPLICANT: ISONO, YUUKO  
 / APPLICANT: HIO, YURI  
 / APPLICANT: OTSUKA, KAORU  
 / APPLICANT: NAGAI, KEIICHI  
 / APPLICANT: IRIE, RYOTARO  
 / APPLICANT: TAMECHIKA, ICHIRO  
 / APPLICANT: SEKI, NAOHICO  
 / APPLICANT: YOSHIKAWA, TSUTOMU  
 / APPLICANT: OTSUKA, MOTOKUKI  
 / APPLICANT: NAGAHARI, KENJI  
 / APPLICANT: MASUHO, YASUHIKO  
 / TITLE OF INVENTION: Novel full length cDNA  
 / FILE REFERENCE: 084335-0191  
 / CURRENT APPLICATION NUMBER: US/11/072,512  
 / CURRENT FILING DATE: 2005-03-07  
 / PRIOR APPLICATION NUMBER: US 60/350,978  
 / PRIOR FILING DATE: 2002-01-25  
 / PRIOR APPLICATION NUMBER: JP 2001-379298  
 / PRIOR FILING DATE: 2001-11-05  
 / NUMBER OF SEQ ID NOS: 4096  
 / SOFTWARE: PatentIn Ver. 2.1  
 / SEQ ID NO 959  
 / LENGTH: 3052  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / US-11-072-512-959

Alignment Scores:  
 Pred. No.: 1,23e-23 Length: 3052  
 Score: 503.00 Matches: 190  
 Percent Similarity: 35.5% Conservative: 83  
 Best Local Similarity: 24.7% Mismatches: 265  
 Query Match: 13.3% Indels: 232  
 DB: 9 Gaps: 34

US-10-755-889-18 (1-706) x US-11-072-512-959 (1-3052)

QY 33 AspValValIleValSerArgIleGlnPheArgAlaHisIleThrValIleuMetAla 52  
 DB 294 GATGTGGCTGTGCTTCTTCCAGGAGGAAGTGGCA-----CTGCTGATCTTACC 344  
 QY 53 CysSerGlyLeuPheTySerIlePheThrAspGlnLeuIleCysAsnLeuSerValIle 72  
 DB 345 CAGAGGAAGCTGTACCGAGATGTCATGTGGAGAACTTCAAG---AACCTGTTGCAAGTG 401  
 QY 73 AsnLeuAspProGlnIleAsnProGlnIlePheCysIleLeuLeuAspPheMetIleThr 92  
 DB 402 GGGCATCTTCCC---TTCCAAACCAAGAT-----ATGGTA 431  
 QY 93 SerArgLeuAsnLeuArgIleGlnIleMetAlaValMetAlaThrAlaMetIleu 112  
 DB 432 TCCCAATTGGAAAGCAAGAAAGCTTTGGATGATGAAACCAAGAAAGCAAGC 491  
 QY 113 GlnMetGlnHisValIleAspThrCysArgIlePhe-----124  
 DB 492 AAGCATCAAAATTAAGATGAAACACTCCAAAAATTGGATTAAATACCTTCAATCA 551

QY 124 -----124  
 DB 552 GAGCTGCTGTGGCAAACTGGAAACAGTTGCAAGTAAATCAAGTCTTCAG 611  
 QY 125 -----132  
 DB 612 GGGAAAGTTCCAGTTATTACAGGTGACTTATTCAGGTTCTGAAAATGGAACAAT 671  
 QY 133 -----143  
 DB 672 ATTAATGACCTTAAGAGATAGCTCTATTATTAATGAAAATCAAGATTTCATTTGG 731  
 QY 144 -----158  
 DB 732 AGAACCCAGCATTTCTGGGGAATACATATCTAGTAGTCACAGATTCCAGAGT--AGA 788  
 QY 159 GlyArgGlnVal---ValGluAsnAsnLeuPro-----LeuArgSerAla 172  
 DB 789 GGTAAAGCAATTATGAAAAATTAACCTGCAAAATCATGAAGACTTCATGAAGAAATCA 848  
 QY 173 ProGlyCysGluSerArgAlaPheAlaProSerLeuTySerGlyLeuSerThrProPro 192  
 DB 849 CCA-----TTTCATGACATATTAAACTGACACAGAACCAAAACC 890  
 QY 193 AlaSerTySerMetTySerHisLeuProValSerSerLeuPheSerAspGlnGlu 212  
 DB 891 TGCAAAGTAAATGATATGGCAAA-----ATCATTTAGTATGGCTCC 932  
 QY 213 PheArgAspValArgMetProValAlaAsnProPheProIleGlnArgAlaLeuProCys 232  
 DB 933 -----AACCAGAATTAACCTTAGA-----GAGAAACCCCATTCAGT 971  
 QY 233 AspSerAlaArgProValProGlyGluTySerArg-----ProThrLeu 247  
 DB 972 -----GGTAGCTGGAAGAGGGCTTCAGTTATAGCCCAAGCTT 1010  
 QY 248 GluValSerProAsnVal-----Cys-----HisSerAsnIleTy 259  
 DB 1011 CCCCTTATCCGATGTTTACACAGAGAAAAATGCTTCACTCAAGCTCAATCTCGA 1070  
 QY 260 SerProIleGlnThrIleProGlnGlnAlaArgSerAspMetHisTySerValAlaGlu 279  
 DB 1071 ACTCATCAGAGAAATTCACCCAGAGAGAAATCAATGATGATGATGATGATGATGATGC 1130  
 QY 280 GlyLeuAspProAlaAlaProSerAlaArgAsn-----AlaProTyPhePro 295  
 DB 1131 TTCAATTAAGAGCTCTTTTCAATTTCTTATCAATCTATATACAGAGAGAAATCTTATAGA 1190  
 QY 296 CysAspIleAsnIleSerIleGlnGlnIleArgProSerSerGlnAspGlnIleAlaLeuHis 315  
 DB 1191 TCGGACAGTTGGCGCAAGGATTC-----AGTAGCAGACAGCGGTCTTATCATTCAT 1241  
 QY 316 PheGlnProProAsnAlaProLeuAsnArgIleGlyLeuValSerProGlnSerProGln 335  
 DB 1242 TACGAACATCATCTGGA-----GAGAAACCTCAT 1271  
 QY 336 LysSerAspCysGlnProAsnSerProThrGlnAlaCysSerSerIleAsnAlaCysIle 355  
 DB 1272 AAA-----TCCAGAGAAATGTGAAATGCTTT 1298  
 QY 356 LeuGlnAlaSerGly-----SerProProAlaLys 365  
 DB 1299 AGTCAAAGTTCAATTTTCAAGTCATCAGAGATCCACACTGAAGAAACCATACAA 1358  
 QY 366 SerProThrAspProIleValCysAsnTrpIleValSerPheIleValLeuAsnSer 385  
 DB 1359 TGCAGAGAGTGTGTAAGGCTTCGTTGG-----AGT 1391  
 QY 386 LeuAsnGlnAsnAlaLysProGlyGlyProGlnGlnAlaGluLeuGlyArgLeuSerPro 405  
 DB 1392 GTTATCTC-----CGTGTTCACAG 1412  
 QY 406 ArgAlaTyThrAlaProProAlaCysGlnProProMetGluProGluAsnLeuAspLeu 425

Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 12 Gaps: 0  
 US-10-755-889-18 (1-706) x US-11-122-329-70 (1-3536)

QY 1 MetAlaSerProAlaAspSerCysIleGlnPheThrArgHisAlaSerAspValLeuLeu 20  
 DB ATGGCTCCCGCGCTGACAGCTGTATCCAGTTTCAACCCCGCATCCAGTGTATCTTCTTC 387  
 QY 21 AsnLeuAsnArgLeuArgSerArgAspIleLeuThrAspValValIleValValSerArg 40  
 DB AACCTTAATCTCTCCGAGTCCAGACATCTTGAATGATGTGTCAATGTGTGACCCG 447  
 QY 41 GluGlnPheArgHisIleValThrValLeuMetAlaCysSerGlyLeuPheTyrSerIle 60  
 DB GAGCACTTTAGACCCCATTAACAGTCTCATATGCGCTGAGTGGCTGTTCTATACATC 507  
 QY 61 PheThrAspGlnLeuLysCysAsnLeuSerValIleAsnLeuAspProGluIleAsnPro 80  
 DB TTTACAGACACAGTTGAATGCAACTTATGATGATCATCTAGATCTCGATCAACCTCT 567  
 QY 81 GluGlyPheCysIleLeuLeuAspPheMetTyrThrSerArgLeuAsnLeuArgGluGly 100  
 DB GAGGAGTTCTGCATCTCTCTGACCTTCAATGATACACATCTCGCTCAATTTGGCGAGG 627  
 QY 101 AsnIleMetAlaValMetAlaThrAlaMetTyrLeuGlnMetGluHisValValAspThr 120  
 DB AACATCATGGCTGTGATGCGCAAGCTATGTACTGTCAGATGAGCATGTGTGACACT 687  
 QY 121 CysArgLeuPheIleLeuValAspSerGluValGluMetValSerAlaIleLysProArg 140  
 DB TGCCGGAATTTTATTAAGCCAGTGAAGAGATGTTTCTGCCATCAAGCTCTCTCGT 747  
 QY 141 GluGlnPheLeuAsnSerArgMetLeuMetProGluAspIleMetAlaTyrArgGlyArg 160  
 DB GAAGAGTTCTCTCAACAGCCGAGATGCTGATCCCCAAGACATCATGCTTACGAGGCT 807  
 QY 161 GluValValGluAsnLeuLeuProLeuArgSerAlaProGlyCysGluSerArgAlaPhe 180  
 DB GAGGTGTGAGAAACAACCTGCCATGAGAGGCGCCCTGGGTGAGACAGACCTTT 867  
 QY 181 AlaProSerLeuTyrSerGlyLeuSerThrProProAlaSerTyrSerMetTyrSerHis 200  
 DB GCCCCAGCCTGTAGATGCTGTCCACACCCGACCTCTTATTCATGTCAGACGAC 927  
 QY 201 LeuProValSerSerLeuLeuPheSerAspGluGlnPheArgAspValArgMetProVal 220  
 DB CTCCCTGTGACAGCTCTCTCTCTCCGATGAGAGATTGCGGATGTCCGATGCTGTG 987  
 QY 221 AlaAsnProPheProLysGluArgAlaLeuProCysAspSerAlaArgProValProGly 240  
 DB GCCAACCTCTTCCCAAGAGCGGCGACCTCCATGTATAGTCCAGGCCAGTCCCTGT 1047  
 QY 241 GluTyrSerArgProThrLeuGluValSerProAsnValCysHisSerAsnIleTyrSer 260  
 DB GAGTACAGCGCGCGACTTGTGAGTGTCCCAATGTGTGCCACAGCAATATCTATTTCA 1107  
 QY 261 ProLysGluThrIleProGluGluValArgSerAspMetHisTyrSerValAlaGluGly 280  
 DB CCCAAGAGAAACATCCAGAGAGGACAGAGATGATGCACTACATGTGCGCTGAGGCG 1167  
 QY 281 LeuLysProAlaAlaProSerAlaArgAsnAlaProTyrPheProCysAspLysAlaSer 300  
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 QY 301 LysGluGluGluArgProSerSerGluAspGluIleAlaLeuHisPheGluProProAsn 320  
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 QY 321 AlaProLeuAsnArgLysGlyLeuValSerProGlnSerProGluLysSerAspCysGln 340  
 DB GCACCTCTGAACCGGAGGCTGTGTTATGTCACAGAGCCCGCAAAATCTGATGCTGAG 1347

QY 341 ProAsnSerProThrGluAlaCysSerSerLysAsnAlaCysIleLeuGlnAlaSerGly 360  
 DB CCCAATCGGCCACAGAGCGCTGCGAGAGTGAAGATGCTGTGATCTCTCAGGCTTCTGCG 1407  
 QY 361 SerProProAlaLysSerProThrAspProLysAlaCysAsnTyrLysIleTyrLysPhe 380  
 DB TCCCTCTCAAGCCAAAGGCCCACTGACCTTCCACTGGAAGAAATCAAGTTTC 1467  
 QY 1408 TCCCTCTCAAGCCAAAGGCCCACTGACCTTCCACTGGAAGAAATCAAGTTTC 1467  
 QY 381 IleValLeuAsnSerLeuAsnGlnAsnAlaLysProGlyGlyProGluGlnAlaGluLeu 400  
 DB ATCGTGTCTCAAGCTCTCAACAGATGCCAAACAGGGGGGCTGAGAGGCTGAGCTG 1527  
 QY 401 GlyArgLeuSerProArgAlaTyrThrAlaProProAlaCysGlnProMetGluPro 420  
 DB GGCCCGCTTCCCAAGAGCTTACAGCGGCCCACTGTGCTGCAACCCCAATGAGGCT 1587  
 QY 421 GluAsnLeuAspLeuGlnSerProThrLysLeuSerAlaSerGlyGluAspSerThrIle 440  
 DB GAAACCTTGACCTTCAAGTCCCAACAGTGAATGCGGAGGAGGACTTCCACATC 1647  
 QY 1588 GAAACCTTGACCTTCAAGTCCCAACAGTGAATGCGGAGGAGGACTTCCACATC 1647  
 QY 441 ProGlnAlaSerArgLeuAsnAsnIleValAsnArgSerMetThrGlySerProArgSer 460  
 DB CCACAGCCAGCGGCTCAATACATCGTTACAGTTCATGACGAGGCTCTCCCGCAGC 1707  
 QY 1648 CCACAGCCAGCGGCTCAATACATCGTTACAGTTCATGACGAGGCTCTCCCGCAGC 1707  
 QY 461 SerSerGluSerHisSerProLeuTyrMetHisProProLysCysThrSerCysGlySer 480  
 DB ACACAGCGAGGACCTCACTCACTTACATGACACCCCGCAAGTGAACGCTCTCGCGCTCT 1767  
 QY 1708 ACACAGCGAGGACCTCACTCACTTACATGACACCCCGCAAGTGAACGCTCTCGCGCTCT 1767  
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 DB CAGTCCCAACAGACAGAGATGCTCTCCACACCGCTGCGGCCCACTTCCAGAGAG 1827  
 QY 1768 CAGTCCCAACAGACAGAGATGCTCTCCACACCGCTGCGGCCCACTTCCAGAGAG 1827  
 QY 501 MetGlyGluThrGlnSerGluTyrSerAspSerSerCysGluAsnGlyAlaPhePheCys 520  
 DB ATGGAGAGAGACCAAGTGTGATGATCAATTTACTGCTGAGAAAGGGGCTTCTTCTG 1887  
 QY 1828 ATGGAGAGAGACCAAGTGTGATGATCAATTTACTGCTGAGAAAGGGGCTTCTTCTG 1887  
 QY 521 AsnGluCysAspCysArgPheSerGluGluValAspLeuLysArgHisThrLeuGlnThr 540  
 DB AATGATGTGATGCTGCGCTCTCTCTGAGGCTCTCACTCAAGAGCACAGCTGACAGAC 1947  
 QY 1888 AATGATGTGATGCTGCGCTCTCTCTGAGGCTCTCACTCAAGAGCACAGCTGACAGAC 1947  
 QY 541 HisSerAspLysProTyrLysCysAspArgCysGlnAlaSerPheArgTyrLysGluAsn 560  
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 QY 1948 CACAGTGAACAACTTCAAGATGTACCGCTCCAGGCTCTTCCGCTTCAAGAGGCAAC 2007  
 QY 561 LeuAlaSerHisLysThrValHisThrGlyGluLysProTyrArgCysAsnIleCysGly 580  
 DB CTGCCAGGACAAAGACGCTCCATACCGGTGAGAAACCTTACGTTGCAACATCTGTGG 2067  
 QY 2008 CTGCCAGGACAAAGACGCTCCATACCGGTGAGAAACCTTACGTTGCAACATCTGTGG 2067  
 QY 581 AlaGlnPheAsnArgProAlaAsnLeuLysThrHisThrArgIleHisSerGlyGluLys 600  
 DB GCCCAGTTCAACCGGCAACGCAACCTGAAACCCACACTGAAATCACTCTGAGAGAG 2127  
 QY 2068 GCCCAGTTCAACCGGCAACGCAACCTGAAACCCACACTGAAATCACTCTGAGAGAG 2127  
 QY 601 ProTyrLysCysGluThrCysGlyValaArgPheValGlnValAlaHisLeuArgAlaHis 620  
 DB CCTTCAAAATGGAACCTGCGAGCGAGATTTGTACAGATGACCCACTTCCGTGCCAT 2187  
 QY 2128 CCTTCAAAATGGAACCTGCGAGCGAGATTTGTACAGATGACCCACTTCCGTGCCAT 2187  
 QY 621 ValLeuIleHisThrGlyGluLysProTyrProCysGluIleCysGlyThrArgPheArg 640  
 DB GTGCTTATCAACACTGTGTAGAGAGCTTATCCCTGTGAATGTGTGTGACCCGTTCCG 2247  
 QY 2188 GTGCTTATCAACACTGTGTAGAGAGCTTATCCCTGTGAATGTGTGTGACCCGTTCCG 2247  
 QY 641 HisLeuGlnThrLeuLysSerHisLeuArgIleHisThrGlyGluLysProTyrHisCys 660  
 DB CACCTTCAACACTGTGAAGAGCACTGCAATTCACACAGAGAGAGAACTTACCACTTGT 2307  
 QY 2248 CACCTTCAACACTGTGAAGAGCACTGCAATTCACACAGAGAGAGAACTTACCACTTGT 2307  
 QY 661 GluLysCysAsnLeuHisPheArgHisIleLysSerGlnLeuArgLeuHisLeuArgGlnLys 680  
 DB GAGAAATGTAACTGTGATTTCCGTCAAAAGCCAGCTGCACTTCACTTGGCCAGAG 2367  
 QY 2308 GAGAAATGTAACTGTGATTTCCGTCAAAAGCCAGCTGCACTTCACTTGGCCAGAG 2367  
 QY 681 HisGlyAlaIleThrAsnThrLysValGlnTyrArgValSerAlaThrAspLeuProPro 700  
 DB CATGGGCGCATACCAACAGCAAGAGTGCATACCGGCTGTGACGACCTGACCTGCTCG 2427  
 QY 2368 CATGGGCGCATACCAACAGCAAGAGTGCATACCGGCTGTGACGACCTGACCTGCTCG 2427

GenCore version 5.1.7  
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## OM protein - nucleic search, using frame\_plus.p2n model

Run on: March 2, 2006, 02:10:16 ; Search time 582 Seconds  
(without alignments)  
2659.480 Million cell updates/sec

Title: US-10-755-889-18  
Perfect score: 3793  
Sequence: 1 MASPADSCIFTRHNSDVL.....TKQYRVNSATDLPPLPKAC 706

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7218512 seqs, 1096188070 residues

Total number of hits satisfying chosen parameters: 14437024

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/abses/ASSSWEB.spool/US10755889/rnat.01032006.143957.11563/app\_query.fasta.1  
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rmpbn -MINMATCH=0.1  
-LOOPC=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blomsum62  
-TRANS=human40.cdi -LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abses06p  
-USER=US10755889 @CGN 1.1 335 @rnat.01032006.143957.11563 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-MAYR TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:\*

1: /cgn2\_6/ptodata/1/pubpna/US08 NEW PUB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/US07 NEW PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US07 NEW PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW PUB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US09 NEW PUB.seq:\*  
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8: /cgn2\_6/ptodata/1/pubpna/US10 NEW PUB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US11 NEW PUB.seq:\*  
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12: /cgn2\_6/ptodata/1/pubpna/US11 NEW PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US60 NEW PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	3793	100.0	3536	12	US-11-122-329-70
2	503	13.3	3052	9	US-11-072-512-959
3	475	12.5	2435	12	US-11-000-688-1136
4	474.5	12.5	2784	9	US-11-072-512-1944

5	473	12.5	3090	9	US-11-072-512-191	Sequence 191, App
6	472.5	12.5	1578	12	US-11-136-527-2436	Sequence 2436, App
7	468.5	12.4	2110	9	US-11-072-512-1778	Sequence 1778, App
8	465.5	12.3	3026	9	US-11-072-512-967	Sequence 967, App
9	465	12.3	3078	9	US-11-072-512-622	Sequence 622, App
10	464	12.2	2724	9	US-11-072-512-1127	Sequence 1127, App
11	464	12.2	2744	7	US-10-517-151-3	Sequence 3, App1
12	463.5	12.2	2241	9	US-11-072-512-693	Sequence 693, App
13	462.5	12.2	2467	9	US-11-072-512-470	Sequence 470, App
14	462.5	12.2	2634	9	US-11-072-512-816	Sequence 816, App
15	462	12.2	4305	8	US-10-750-185-44166	Sequence 44166, A
16	462	12.2	4305	8	US-10-750-623-44166	Sequence 44166, A
17	461.5	12.2	1833	9	US-11-072-512-1491	Sequence 1491, App
18	460.5	12.1	3335	9	US-11-072-512-522	Sequence 522, App
19	459.5	12.1	2918	9	US-11-072-512-835	Sequence 835, App
20	458	12.1	1914	9	US-11-072-512-1464	Sequence 1464, App
21	457.5	12.1	2603	12	US-11-000-688-1179	Sequence 1179, App
22	457.5	12.1	193789	12	US-11-112-908-55	Sequence 55, App1
23	457	12.0	1694	9	US-11-072-512-1500	Sequence 1500, App
24	456.5	12.0	648	6	US-09-925-065A-418152	Sequence 418152, A
25	454.5	12.0	2509	6	US-09-925-065A-87059	Sequence 87059, A
26	454.5	12.0	2537	9	US-11-072-512-1179	Sequence 1179, App
27	454.5	12.0	3138	9	US-11-072-512-83	Sequence 83, App1
28	454	12.0	3301	9	US-11-072-512-479	Sequence 479, App
29	453.5	12.0	648	6	US-09-925-065A-418150	Sequence 418150, A
30	450.5	11.9	648	6	US-09-925-065A-418151	Sequence 418151, A
31	450.5	11.9	2042	9	US-11-072-512-1396	Sequence 1396, App
32	450.5	11.9	3400	9	US-11-072-512-1037	Sequence 1037, App
33	450	11.9	3492	6	US-09-925-065A-47571	Sequence 47571, A
34	450	11.9	3492	6	US-09-925-065A-47572	Sequence 47572, A
35	449.5	11.9	2252	8	US-10-750-185-58156	Sequence 58156, A
36	449.5	11.9	2252	8	US-10-750-623-58156	Sequence 58156, A
37	449	11.8	600	12	US-11-136-527-6532	Sequence 6532, App
38	448	11.8	2985	12	US-11-122-329-116	Sequence 116, App
39	447.5	11.8	2357	9	US-11-072-512-1701	Sequence 1701, App
40	446.5	11.8	2668	12	US-11-136-527-2016	Sequence 2016, App
41	445	11.7	2698	9	US-11-072-512-271	Sequence 271, App
42	445	11.7	2857	12	US-11-136-527-360	Sequence 360, App
43	443.5	11.7	2509	6	US-09-925-065A-87058	Sequence 87058, A
44	442.5	11.7	732	6	US-09-925-065A-918557	Sequence 918557, A
45	442.5	11.7	732	6	US-09-925-065A-918560	Sequence 918560, A

## ALIGNMENTS

RESULT 1  
US-11-122-329-70  
; Sequence 70, Application US/11122329  
; Publication No. US20060019272A1  
; GENERAL INFORMATION:  
; APPLICANT: Geraci, Mark  
; APPLICANT: Bull, Todd  
; APPLICANT: Voelkel, Norbert  
; APPLICANT: Coldren, Chris  
; TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gene  
; FILE REFERENCE: 2448-54  
; CURRENT APPLICATION NUMBER: US/11/122,329  
; PRIOR FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/568,129  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 70  
; LENGTH: 3536  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-122-329-70  
Alignment Scores:  
Pred. No.: 6.47e-240 Length: 3536  
Score: 3793.00 Matches: 706  
Percent Similarity: 100.0% Conservative: 0

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 2, 2006, 03:45:47 ; Search time 187 Seconds  
(without alignments)  
1658.831 Million cell updates/sec

Title: US-10-755-889-18

Sequence: 1 MASPADSCIOFTTHASDVLL.....TKVQVRVSATDLPPELPKAC 706

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: A\_Geneseq\_21.\*
- 2: geneseqp1980s.\*
- 3: geneseqp1990s.\*
- 4: geneseqp2000s.\*
- 5: geneseqp2001s.\*
- 6: geneseqp2002s.\*
- 7: geneseqp2003s.\*
- 8: geneseqp2004s.\*
- 9: geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3793	100.0	706	3	AAy78793 Human BCL
2	3793	100.0	706	4	AAy78793 Human BCL
3	3793	100.0	706	8	ADL82847 Human PRO
4	3793	100.0	706	8	ADL82847 Human PRO
5	3793	100.0	706	8	ADL82847 Human PRO
6	3777	99.6	706	9	ADL14017 Human NF-
7	3777	99.6	706	9	ADL14017 Human NF-
8	3777	99.6	706	9	ADL14017 Human NF-
9	3771	99.4	706	7	ADJ70182 Human hea
10	3763	99.2	706	2	AAy78793 Human BCL
11	3763	99.2	706	3	AAy78793 Human BCL
12	3602.5	95.0	707	5	ABW57289 Mouse lsc
13	3602.5	95.0	707	5	ABW57289 Mouse lsc
14	3602.5	95.0	707	5	ABW57289 Mouse lsc
15	3602.5	95.0	707	5	ABW57289 Mouse lsc
16	3602.5	95.0	707	5	ABW57289 Mouse lsc
17	3602.5	95.0	707	5	ABW57289 Mouse lsc
18	3602.5	95.0	707	5	ABW57289 Mouse lsc
19	3602.5	95.0	707	5	ABW57289 Mouse lsc
20	3602.5	95.0	707	5	ABW57289 Mouse lsc
21	3602.5	95.0	707	5	ABW57289 Mouse lsc
22	3602.5	95.0	707	5	ABW57289 Mouse lsc
23	3602.5	95.0	707	5	ABW57289 Mouse lsc
24	3602.5	95.0	707	5	ABW57289 Mouse lsc

25	618.5	16.3	810	3	AAy73351	AAy73351 HTRM clon
26	610	16.1	803	7	ADD45510	ADD45510 Human pro
27	610	16.1	803	8	ADD45510	ADD45510 Human pro
28	609	16.1	803	4	AAy73351	AAy73351 HTRM clon
29	609	16.1	804	4	AAy73351	AAy73351 HTRM clon
30	602	15.9	803	2	AAy73351	AAy73351 HTRM clon
31	602	15.9	803	2	AAy73351	AAy73351 HTRM clon
32	588	14.9	765	6	ADP96329	ADP96329 Human nuc
33	564.5	14.9	765	6	ADP96329	ADP96329 Human nuc
34	560	14.8	765	6	ADP96329	ADP96329 Human nuc
35	540	14.2	688	5	ABW57289	ABW57289 Mouse lsc
36	535	14.1	775	7	ADC31774	ADC31774 Human nov
37	522.5	13.8	603	4	AAy73351	AAy73351 HTRM clon
38	522.5	13.8	610	4	AAy73351	AAy73351 HTRM clon
39	522.5	13.8	610	4	AAy73351	AAy73351 HTRM clon
40	522.5	13.8	610	4	AAy73351	AAy73351 HTRM clon
41	522.5	13.8	610	5	AAy73351	AAy73351 HTRM clon
42	522.5	13.8	610	5	AAy73351	AAy73351 HTRM clon
43	518	13.7	706	9	ADY71947	ADY71947 Mouse GZF
44	517	13.6	711	5	AAO21779	AAO21779 Lung-spec
45	517	13.6	711	9	ADY71945	ADY71945 Human GZF

## ALIGNMENTS

### RESULT 1

AAy78793 standard; protein; 706 AA..

AAy78793;

19-MAY-2000 (first entry)

Human BCL-6 protein sequence.

Bcl-6; human; B-cell lymphoma; regulator; non-Hodgkin's lymphoma;

diffuse type B-cell lymphoma.

Homo sapiens.

MO200000185-A1.

06-JUN-2000.

30-JUN-1999; 99MO-US014703.

30-JUN-1998; 98US-00107058.

(UYCO ) UNIV COLUMBIA NEW YORK.

Dalla-Favera R, Niu H;

WPI; 2000-160631/14.

Novel methods for regulating BCL-6 levels in cells used to treat humans with lymphoma.

Example 2; Fig 10; 159pp; English.

This sequence represents the human bcl-6 protein sequence. The invention relates to a vertebrate bcl-6 locus which is the breakpoint cluster region in B-cell lymphomas, and contains a bcl-6 gene encoding a BCL-6 polypeptide. Administration of a molecule which induces phosphorylation of BCL-6 and thereby induces BCL-6 degradation, can be used as a method of regulating BCL-6 in cells. The methods of the invention can be used to regulate, and especially to decrease BCL-6 levels in cells. The methods may also be used to screen putative therapeutic agents for treatment of non-Hodgkin's lymphoma, by contacting cells from lymphoma and normal cells with the agent, and after a period of time comparing the amount of bcl-6 nucleic acid in each sample, a difference indicating the effectiveness of the agent. The bcl-6 gene is a source of probes and primers, which are used to diagnose diffuse-type B cell lymphoma and B

Attachment 1



CC cell lymphoma in a subject. Anti-BCL-6 antibodies may also be used for  
 CC this purpose. The methods are useful for treating non-Hodgkin's lymphoma  
 XX  
 XX  
 SQ Sequence 706 AA;

Query Match 100.0%; Score 3793; DB 3; Length 706;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-284;  
 Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTRHNASDVLNLRNRSRDILTDVIVVSRQFRAHKTVMACSGLPYSI 60  
 DB 1 MASPADSCIOFTRHNASDVLNLRNRSRDILTDVIVVSRQFRAHKTVMACSGLPYSI 60  
 QY 61 FTDLKCNLSVINLDEPINEGFCILDFMTYSRLNLRGINAVATAMTLQMEHVDT 120  
 DB 61 FTDLKCNLSVINLDEPINEGFCILDFMTYSRLNLRGINAVATAMTLQMEHVDT 120  
 QY 121 CRKPTKASEAMVSAIKPREEFLNSRLMPODIMAYRGREVENNLPLRSAPGCSRA 180  
 DB 121 CRKPTKASEAMVSAIKPREEFLNSRLMPODIMAYRGREVENNLPLRSAPGCSRA 180  
 QY 181 APSLYSGISTPSPASYSMTSHLPVSSLLFSDDEFRDVRPVPANPPKRALPCDSAR 240  
 DB 181 APSLYSGISTPSPASYSMTSHLPVSSLLFSDDEFRDVRPVPANPPKRALPCDSAR 240  
 QY 241 EYSRPTLEVS PNVCHSNISPKETIPBEARSDMHYSVABGLKPAASARNAPYPCDKAS 300  
 DB 241 EYSRPTLEVS PNVCHSNISPKETIPBEARSDMHYSVABGLKPAASARNAPYPCDKAS 300  
 QY 301 KEERPRSSSEBIALHFEPPNAPLNKGLVSPQSPQSDCPNSPTKACSKNACILQASG 360  
 DB 301 KEERPRSSSEBIALHFEPPNAPLNKGLVSPQSPQSDCPNSPTKACSKNACILQASG 360  
 QY 361 SPPAKSPTDPKACNMKKYKRTIVNSLNQNAKPGSPROAELGRISPRATYAPACOP 420  
 DB 361 SPPAKSPTDPKACNMKKYKRTIVNSLNQNAKPGSPROAELGRISPRATYAPACOP 420  
 QY 421 ENMDLQSPPTLSASGSDSTIPQASRLNINVRSMTSPSSSSSHSPLVYHPPKCTSCS 480  
 DB 421 ENMDLQSPPTLSASGSDSTIPQASRLNINVRSMTSPSSSSSHSPLVYHPPKCTSCS 480  
 QY 481 OSQOHAEMCLHTAGPTFAEMGTOSHSYSDSCENGAFCNECDCEPSEBASIKRTT 540  
 DB 481 OSQOHAEMCLHTAGPTFAEMGTOSHSYSDSCENGAFCNECDCEPSEBASIKRTT 540  
 QY 541 HSDKPYKCDRCQASFRYKGNLASHKTVHGEKPYRCNICGAQPNRPNALKTHRHIS 600  
 DB 541 HSDKPYKCDRCQASFRYKGNLASHKTVHGEKPYRCNICGAQPNRPNALKTHRHIS 600  
 QY 601 PYKCEITCGARFVQVAHLRAHVLHTEGKPYCEICGTRFRHLQTLKSHLRHTEG 660  
 DB 601 PYKCEITCGARFVQVAHLRAHVLHTEGKPYCEICGTRFRHLQTLKSHLRHTEG 660  
 QY 661 EKCNLHFRKHSQRLRLRQHGAILNTKQVYRSATDLPPELPKAC 706  
 DB 661 EKCNLHFRKHSQRLRLRQHGAILNTKQVYRSATDLPPELPKAC 706

RESULT 2  
 AAB29640  
 ID AAB29640 standard; protein; 706 AA.  
 AC AAB29640;  
 XX  
 XX  
 DT 23-FEB-2001 (first entry)  
 XX  
 DB Human bcl-6 transcriptional repressor.  
 XX  
 KW Human; bcl-6; transcriptional repressor; germinal centre formation;  
 KW Th-2 mediated antibody affinity maturation; apoptosis regulator;  
 KW chromosome 3q27; lymphoma; acute lymphoblastic leukaemia;  
 KW post-transplant lymphoproliferative disorder; expression inhibition;  
 KW antisense therapy.

XX Homo sapiens.  
 OS  
 XX  
 PN US6140125-A.  
 XX  
 PD 31-OCT-2000.  
 XX  
 PF 15-OCT-1999; 99US-00418640.  
 XX  
 PR 15-OCT-1999; 99US-00418640.  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Taylor JK, Cowsett LM;  
 DR WPI: 2001-048959/06.  
 DR N-PSDB; AAC81137.  
 XX  
 PT Antisense compounds which specifically hybridize with and inhibit human  
 PT bcl-6 expression, useful for treating bcl-6 related disorders, and  
 PT preventing or delaying inflammation or tumor formation.  
 PS Disclosure; Col 47-52; 42pp; English.

CC This sequence represents human bcl-6. Bcl-6 (also known as B-cell  
 CC Ctl/Lymphoma 6, zinc finger protein 51 and LAZ3) is a sequence-specific  
 CC DNA-binding transcriptional repressor. The bcl-6 gene is expressed in  
 CC germinal centre B- and T- cells and is required for germinal centre  
 CC formation and Th-2 mediated antibody affinity maturation. Bcl-6 may also  
 CC play a role in the regulation of apoptosis. The bcl-6 gene is located on  
 CC chromosome 3q27, a region which undergoes a high frequency of  
 CC translocation events. Such chromosomal translocations can result in  
 CC aberrant forms of bcl-6, which are strongly implicated in the  
 CC pathogenesis of several types of lymphoma, and have also been reported in  
 CC acute lymphoblastic leukaemia and post-transplant lymphoproliferative  
 CC disorders. The invention relates to antisense oligonucleotides targeted  
 CC to the human bcl-6 gene, which inhibit its expression. A series of  
 CC oligonucleotides (AAC81144-C81223) were designed to target different  
 CC regions of the human bcl-6 mRNA, and were analysed for their effect on  
 CC bcl-6 mRNA levels by quantitative real-time PCR. The oligonucleotides of  
 CC the invention are useful for diagnosis, prevention and treatment of  
 CC conditions associated with aberrant forms of bcl-6, such as lymphomas,  
 CC acute lymphoblastic leukaemia and post-transplant lymphoproliferative  
 CC disorders

XX  
 SQ Sequence 706 AA;  
 Query Match 100.0%; Score 3793; DB 4; Length 706;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-284;  
 Matches 706; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPADSCIOFTRHNASDVLNLRNRSRDILTDVIVVSRQFRAHKTVMACSGLPYSI 60  
 DB 1 MASPADSCIOFTRHNASDVLNLRNRSRDILTDVIVVSRQFRAHKTVMACSGLPYSI 60  
 QY 61 FTDLKCNLSVINLDEPINEGFCILDFMTYSRLNLRGINAVATAMTLQMEHVDT 120  
 DB 61 FTDLKCNLSVINLDEPINEGFCILDFMTYSRLNLRGINAVATAMTLQMEHVDT 120  
 QY 121 CRKPTKASEAMVSAIKPREEFLNSRLMPODIMAYRGREVENNLPLRSAPGCSRA 180  
 DB 121 CRKPTKASEAMVSAIKPREEFLNSRLMPODIMAYRGREVENNLPLRSAPGCSRA 180  
 QY 181 APSLYSGISTPSPASYSMTSHLPVSSLLFSDDEFRDVRPVPANPPKRALPCDSAR 240  
 DB 181 APSLYSGISTPSPASYSMTSHLPVSSLLFSDDEFRDVRPVPANPPKRALPCDSAR 240  
 QY 241 EYSRPTLEVS PNVCHSNISPKETIPBEARSDMHYSVABGLKPAASARNAPYPCDKAS 300  
 DB 241 EYSRPTLEVS PNVCHSNISPKETIPBEARSDMHYSVABGLKPAASARNAPYPCDKAS 300  
 QY 301 KEERPRSSSEBIALHFEPPNAPLNKGLVSPQSPQSDCPNSPTKACSKNACILQASG 360  
 DB 301 KEERPRSSSEBIALHFEPPNAPLNKGLVSPQSPQSDCPNSPTKACSKNACILQASG 360

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